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(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

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(54) Title: METHOD FOR DISTINGUISHING AML SUBTYPES WITH DIFFERENTS GENE DOSAGES

(57) Abstract: Disclosed is a method for distinguishing AML subtypes with different gene dosages selected from AML-TRI8-AML-TRI11-AML-TRI13, AML-,MO7, and/or AML-DEL5q in a sample by determinig the expression level of markers, as well as a diagnostic kit and an apparatus containing the markers.

INTERNATIONAL SEARCH REPORT

International Application No
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A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 G01N33/574 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 G01N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
EPO-Internal, BIOSIS, WPI Data, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	VIRTANEVA K ET AL: "EXPRESSION PROFILING REVEALS FUNDAMENTAL BIOLOGICAL DIFFERENCES IN ACUTE MYELOID LEUKEMIA WITH ISOLATED TRISOMY 8 AND NORMAL CYTOGENETICS" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 98, no. 3, 30 January 2001 (2001-01-30), pages 1124-1129, XP002952627 ISSN: 0027-8424 cited in the application the whole document ----- -/--	1-27

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
2 March 2005	13. 07. 2005

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Thumb, W

Form PCT SA/210 (second sheet) (January 2004)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	QIAN ZHIJIAN ET AL: "Expression profiling of CD34+ hematopoietic stem/ progenitor cells reveals distinct subtypes of therapy-related acute myeloid leukemia" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 99, no. 23, 12 November 2002 (2002-11-12), pages 14925-14930, XP002261373 ISSN: 0027-8424 abstract page 14927, column 2	1-27
Y	WO 03/039443 A (DEUTSCHES KREBSFORSCH ;HAFERLACH TORSTEN (DE); EILS ROLAND (DE); K) 15 May 2003 (2003-05-15) the whole document in particular Example 7, page 125	1-27
Y	DATABASE BIOSIS [Online] BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2001 (2001-11-16), CHEN GUIBIN ET AL: "Distinct gene expression profile in CD34 cells from patients with specific karyotypic defects in myelodysplasia" XP002273025 Database accession no. PREV200200250081 abstract & BLOOD, vol. 98, no. 11 Part 1, 16 November 2001 (2001-11-16), pages 728a-729a, 43rd Annual Meeting of the American Society of Hematology, Part 1;Orlando, Florida, USA; December 07-11, 2001 ISSN: 0006-4971	1-27
Y	DATABASE BIOSIS [Online] BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2002 (2002-11-16), VEY NORBERT ET AL: "Gene Expression Profiling of Acute Myeloid Leukemias with Normal Karyotype." XP002273026 Database accession no. PREV200300357083 abstract -/--	1-27

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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Y	DATABASE BIOSIS [Online] BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2002 (2002-11-16), QIAN ZHIJIAN ET AL: "Expression Profiling of CD34+ Hematopoietic Progenitors Reveals Distinct Subtypes of Therapy-Related Acute Myeloid Leukemia." XP002273027 Database accession no. PREV200300335806 abstract & BLOOD, vol. 100, no. 11, 16 November 2002 (2002-11-16), page Abstract No. 1206, 44th Annual Meeting of the American Society of Hematology;Philadelphia, PA, USA; December 06-10, 2002 ISSN: 0006-4971 -----	1-27
Y	DATABASE BIOSIS [Online] BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2002 (2002-11-16), RITTER MARKUS ET AL: "Differentially Regulated Signaling Pathways in AML with Monosomy 7 and 7q-." XP002273028 Database accession no. PREV200300367793 abstract & BLOOD, vol. 100, no. 11, 16 November 2002 (2002-11-16), page Abstract No. 4309, 44th Annual Meeting of the American Society of Hematology;Philadelphia, PA, USA; December 06-10, 2002 ISSN: 0006-4971 -----	1-27
Y	EP 1 043 676 A (WHITEHEAD BIOMEDICAL INST) 11 October 2000 (2000-10-11) the whole document -----	1-27
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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	GOLUB T R ET AL: "Molecular classification of cancer: Class discovery and class prediction by gene expression monitoring" SCIENCE, AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE,, US, vol. 286, no. 5439, 15 October 1999 (1999-10-15), pages 531-537, XP002207658 ISSN: 0036-8075 cited in the application the whole document	1-27
Y	DATABASE BIOSIS [Online] BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2002 (2002-11-16), KOHLMANN ALEXANDER ET AL: "A Simplified and Partially Automated Target Preparation Method for Gene Expression Profiling." XP002269495 Database accession no. PREV200300367771 abstract & BLOOD, vol. 100, no. 11, 16 November 2002 (2002-11-16), page Abstract No. 4287, 44th Annual Meeting of the American Society of Hematology;Philadelphia, PA, USA; December 06-10, 2002 ISSN: 0006-4971	1-27
Y	HAFERLACH T ET AL: "The Diagnosis of 14 Specific Subtypes of Leukemia Is Possible Based on Gene Expression Profiles: A Study on 263 Patients with AML, ALL, CML, or CLL" BLOOD, W.B.SAUNDERS COMPAGNY, ORLANDO, FL, US, vol. 100, no. 11, 16 November 2002 (2002-11-16), page 139A, XP002263227 ISSN: 0006-4971 the whole document	1-27
Y	KOHLMANN A ET AL: "MOLECULAR CHARACTERIZATION OF ACUTE LEUKEMIAS BY USE OF MICROARRAY TECHNOLOGY" GENES, CHROMOSOMES & CANCER, XX, XX, vol. 37, no. 4, August 2003 (2003-08), pages 396-405, XP008025253 the whole document	1-27

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	DUGAS MARTIN ET AL: "Impact of integrating clinical and genetic information." IN SILICO BIOLOGY, vol. 2, no. 3, 2002, pages 383-391, XP001179418 ISSN: 1386-6338 (ISSN print) the whole document	1-27
Y	DUGAS M ET AL: "A comprehensive leukemia database: integration of cytogenetics, molecular genetics and microarray data with clinical information, cytomorphology and immunophenotyping" LEUKEMIA, MACMILLAN PRESS LTD, US, vol. 15, no. 12, December 2001 (2001-12), pages 1805-1810, XP002263731 ISSN: 0887-6924 the whole document	1-27
A	ALIZADEH A ET AL: "THE LYMPHOCHIP: A SPECIALIZED CDNA MICROARRAY FOR THE GENOMIC-SCALE ANALYSIS OF GENE EXPRESSION IN NORMAL AND MALIGNANT LYMPHOCYTES" COLD SPRING HARBOR SYMPOSIA ON QUANTITATIVE BIOLOGY, BIOLOGICAL LABORATORY, COLD SPRING HARBOR, NY, US, vol. 64, no. 1, 1999, pages 71-78, XP001099007 ISSN: 0091-7451 the whole document	1-27
A	WO 03/083140 A (WONG LIMSOON ;YEOH ENG-JUH (SG); DOWNING JAMES R (US); WILKINS DAW) 9 October 2003 (2003-10-09) table 63	1-27

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP2004/012469

Box II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Article 52 (2)(d) EPC - Presentation of information

The claims were only searched with regards to the underlying method of generating a reference data base for distinguishing AML subtypes with

2. [ ] Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [X] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-27 (partially)

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box II.1

Article 52 (2)(d) EPC - Presentation of information

The claims were only searched with regards to the underlying method of generating a reference data base for distinguishing AML subtypes with different gene dosages.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-27 (partially)

A method for distinguishing AML_+11 from AML_TRI+8, AML_TRI+13, AML-MO7, AML-DEL5q, and/or AML-DEL9, the method comprising determining the expression level of the marker ITGAE (CD103). Use of said marker for the manufacture of a diagnostic. A diagnostic kit containing said marker and an apparatus comprising a reference data bank, wherein the reference data bank is obtainable by determining the expression level of ITGAE.

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2. claims: 1-27 (all partially)

Inventions 2-1400

Methods for distinguishing AML subtypes with different gene dosages selected from AML_TRI+8, AML_TRI+11, AML_TRI+13, AML-MO7, AML-DEL5q, and/or AML-DEL9q, and methods for distinguishing specific subtypes against all other AML subtypes and against each other, the methods comprising determining individually the expression level of the markers listed in tables 1.1, positions 2-50, tables 1.2-1.7 and in table 2. Use of said markers for the manufacture of diagnostics. Diagnostic kits containing said markers and apparatus comprising a reference data bank, wherein the reference data bank is obtainable by determining the expression levels of said markers.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No
PCT/EP2004/012469

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 03039443 A	15-05-2003	EP 1308522 A1	07-05-2003
		WO 03039443 A2	15-05-2003
		EP 1470247 A2	27-10-2004
EP 1043676 A	11-10-2000	CA 2304876 A1	09-10-2000
		EP 1043676 A2	11-10-2000
		JP 2001017171 A	23-01-2001
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		WO 03083140 A2	09-10-2003
		US 2004018513 A1	29-01-2004

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Published:
— *without international search report and to be republished upon receipt of that report*

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(57) Abstract: Disclosed is a method for distinguishing AML subtypes with different gene dosages selected from AML-TRI8-AML-TRI11-AML-TRI13, AML-,MO7, and/or AML-DEL5q in a sample by determinig the expression level of markers, as well as a diagnostic kit and an apparatus containing the markers.

WO 2005/043167 A2

Method for distinguishing AML subtypes with different gene dosages

The present invention is directed to a method for distinguishing AML subtypes with different gene dosages selected from AML-TRI8, AML-TRI11, AML-TRI13, AML-MO7, and/or AML-DEL5q by determining the expression level of selected marker genes.

Leukemias are classified into four different groups or types: acute myeloid (AML), acute lymphatic (ALL), chronic myeloid (CML) and chronic lymphatic leukemia (CLL). Within these groups, several subcategories can be identified further using a panel of standard techniques as described below. These different subcategories in leukemias are associated with varying clinical outcome and therefore are the basis for different treatment strategies. The importance of highly specific classification may be illustrated in detail further for the AML as a very heterogeneous group of diseases. Effort is aimed at identifying biological entities and to distinguish and classify subgroups of AML which are associated with a favorable, intermediate or unfavorable prognosis, respectively. In 1976, the FAB classification was proposed by the French-American-British co-operative group which was based on cytomorphology and cytochemistry in order to separate AML subgroups according to the morphological appearance of blasts in the blood and bone marrow. In addition, it was recognized that genetic abnormalities occurring in the leukemic blast had a major impact on the morphological picture and even more on the prognosis. So far, the karyotype of the leukemic blasts is the most important independent prognostic factor regarding response to therapy as well as survival.

Usually, a combination of methods is necessary to obtain the most important information in leukemia diagnostics: Analysis of the morphology and cytochemistry of bone marrow blasts and peripheral blood cells is necessary to establish the diagnosis. In some cases the addition of immunophenotyping is mandatory to separate very undifferentiated AML from acute lymphoblastic leukemia and CLL. Leukemia subtypes investigated can be diagnosed by cytomorphology alone, only if an expert reviews the smears. However, a genetic analysis based on chromosome analysis, fluorescence in situ hybridization or RT-PCR and immunophenotyping is required in order to assign all cases into the right category. The aim of these techniques besides diagnosis is mainly to determine the

prognosis of the leukemia. A major disadvantage of these methods, however, is that viable cells are necessary as the cells for genetic analysis have to divide in vitro in order to obtain metaphases for the analysis. Another problem is the long time of 72 hours from receipt of the material in the laboratory to obtain the result. Furthermore, great experience in preparation of chromosomes and even more in analyzing the karyotypes is required to obtain the correct result in at least 90% of cases. Using these techniques in combination, hematological malignancies in a first approach are separated into chronic myeloid leukemia (CML), chronic lymphatic (CLL), acute lymphoblastic (ALL), and acute myeloid leukemia (AML). Within the latter three disease entities several prognostically relevant subtypes have been established. As a second approach this further sub-classification is based mainly on genetic abnormalities of the leukemic blasts and clearly is associated with different prognoses.

The sub-classification of leukemias becomes increasingly important to guide therapy. The development of new, specific drugs and treatment approaches requires the identification of specific subtypes that may benefit from a distinct therapeutic protocol and, thus, can improve outcome of distinct subsets of leukemia. For example, the new therapeutic drug (STI571, Imatinib) inhibits the CML specific chimeric tyrosine kinase BCR-ABL generated from the genetic defect observed in CML, the BCR-ABL-rearrangement due to the translocation between chromosomes 9 and 22 (t(9;22) (q34; q11)). In patients treated with this new drug, the therapy response is dramatically higher as compared to all other drugs that had been used so far. Another example is the subtype of acute myeloid leukemia AML M3 and its variant M3v both with karyotype t(15;17)(q22; q11-12). The introduction of a new drug (all-trans retinoic acid - ATRA) has improved the outcome in this subgroup of patients from about 50% to 85 % long-term survivors. As it is mandatory for these patients suffering from these specific leukemia subtypes to be identified as fast as possible so that the best therapy can be applied, diagnostics today must accomplish sub-classification with maximal precision. Not only for these subtypes but also for several other leukemia subtypes different treatment approaches could improve outcome. Therefore, rapid and precise identification of distinct leukemia subtypes is the future goal for diagnostics.

Thus, the technical problem underlying the present invention was to provide means for leukemia diagnostics which overcome at least some of the disadvantages of the prior art diagnostic methods, in particular encompassing the time-consuming and unreliable combination of different methods and which provides a rapid assay to unambiguously distinguish one AML subtype from another, e.g. by genetic analysis.

According to Golub et al. (Science, 1999, 286, 531-7), gene expression profiles can be used for class prediction and discriminating AML from ALL samples. However, for the analysis of acute leukemias the selection of the two different subgroups was performed using exclusively morphologic-phenotypical criteria. This was only descriptive and does not provide deeper insights into the pathogenesis or the underlying biology of the leukemia. The approach reproduces only very basic knowledge of cytomorphology and intends to differentiate classes. The data is not sufficient to predict prognostically relevant cytogenetic aberrations.

Furthermore, the international application WO-A 03/039443 discloses marker genes the expression levels of which are characteristic for certain leukemia, e.g. AML subtypes and additionally discloses methods for differentiating between the subtype of AML cells by determining the expression profile of the disclosed marker genes. However, WO-A 03/039443 does not provide guidance which set of distinct genes discriminate between two subtypes and, as such, can be routineously taken in order to distinguish one AML subtype from another.

The problem is solved by the present invention, which provides a method for distinguishing AML subtypes with different gene dosages selected from AML-TRI8, AML-TRI11, AML-TRI13, AML-MO7, and/or AML-DEL5q in a sample, the method comprising determining the expression level of markers selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, and/or 2,

wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.1 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.1 having a positive fc value,

is indicative for the presence of AML_+11 when AML_+11 is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.2 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.2 having a positive fc value,

is indicative for the presence of AML_+13 when AML_+13 is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.3 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.3 having a positive fc value,

is indicative for the presence of AML_+8 when AML_+8 is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.4 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.4 having a positive fc value,

is indicative for the presence of AML_-7 when AML_-7 is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.5 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.5 having a positive fc value,

is indicative for the presence of AML_5q when AML_5q is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.6 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.6 having a positive fc value,

is indicative for the presence of AML_9q when AML_9q is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.7 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.7 having a positive fc value,

is indicative for the presence of AML_normal when AML_normal is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.1 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.1 having a positive fc value,

is indicative for the presence of AML_+11 when AML_+11 is distinguished from AML_+13,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.2 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.2 having a positive fc value,

is indicative for the presence of AML_+11 when AML_+11 is distinguished from AML_+8,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.3 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.3 having a positive fc value,

is indicative for the presence of AML_+11 when AML_+11 is distinguished from AML_-7,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.4 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.4 having a positive fc value,

is indicative for the presence of AML_+11 when AML_+11 is distinguished from AML_5q,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.5 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.5 having a positive fc value,

is indicative for the presence of AML_+11 when AML_+11 is distinguished from AML_9q,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.6 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.6 having a positive fc value,

is indicative for the presence of AML_+11 when AML_+11 is distinguished from AML_normal,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.7 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.7 having a positive fc value,

is indicative for the presence of AML_+13 when AML_+13 is distinguished from AML_+8,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.8 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.8 having a positive fc value,

is indicative for the presence of AML_+13 when AML_+13 is distinguished from AML_-7,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.9 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.9 having a positive fc value,

is indicative for the presence of AML_+13 when AML_+13 is distinguished from AML_5q,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.10 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.10 having a positive fc value,

is indicative for the presence of AML_+13 when AML_+13 is distinguished from AML_9q,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.11 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.11 having a positive fc value,

is indicative for the presence of AML_+13 when AML_+13 is distinguished from AML_normal,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.12 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.12 having a positive fc value,

is indicative for the presence of AML_+8 when AML_+8 is distinguished from AML_-7,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.13 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.13 having a positive fc value,

is indicative for the presence of AML_+8 when AML_+8 is distinguished from AML_5q,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.14 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.14 having a positive fc value,

is indicative for the presence of AML_+8 when AML_+8 is distinguished from AML_9q,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.15 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.15 having a positive fc value,

is indicative for the presence of AML_+8 when AML_+8 is distinguished from AML_normal,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.16 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.16 having a positive fc value,

is indicative for the presence of AML_-7 when AML_-7 is distinguished from AML_5q,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.17 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.17 having a positive fc value,

is indicative for the presence of AML_-7 when AML_-7 is distinguished from AML_9q,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.18 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.18 having a positive fc value,

is indicative for the presence of AML_-7 when AML_-7 is distinguished from AML_normal,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.19 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.19 having a positive fc value,

is indicative for the presence of AML_5q when AML_5q is distinguished from AML_9q,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.20 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.20 having a positive fc value,

is indicative for the presence of AML_5q when AML_5q is distinguished from AML_normal,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.21 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.21 having a positive fc value,

is indicative for the presence of AML_9q when AML_9q is distinguished from AML_normal.

As used herein, the following explanations apply to the above used abbreviations (see also example 1:

1) AML_5q: AML with (5q) deletion
2) AML_9q: AML with (9q) deletion
3) AML_-7: AML with monosomy of chromosome 7 (MO7)
4) AML_+8: AML with trisomy of Chromosome 8 (TRI8)
5) AML_+11: AML with trisomy of chromosome 11 (TRI11)
6) AML_+13: AML with trisomy of chromosome 13
7) AML_normal: AML with normal karyotype

As used herein, "all other subtypes" refer to the subtypes of the present invention, i.e. if one subtype is distinguished from "all other subtypes", it is distiguished from all other subtypes contained in the present invention.

According to the present invention, a "sample" means any biological material containing genetic information in the form of nucleic acids or proteins obtainable or obtained from an individual. The sample includes e.g. tissue samples, cell samples, bone marrow and/or body fluids such as blood, saliva, semen. Preferably,

the sample is blood or bone marrow, more preferably the sample is bone marrow. The person skilled in the art is aware of methods, how to isolate nucleic acids and proteins from a sample. A general method for isolating and preparing nucleic acids from a sample is outlined in Example 3.

According to the present invention, the term "lower expression" is generally assigned to all by numbers and Affymetrix Id. definable polynucleotides the t-values and fold change (fc) values of which are negative, as indicated in the Tables. Accordingly, the term "higher expression" is generally assigned to all by numbers and Affymetrix Id. definable polynucleotides the t-values and fold change (fc) values of which are positive.

According to the present invention, the term "expression" refers to the process by which mRNA or a polypeptide is produced based on the nucleic acid sequence of a gene, i.e. „expression" also includes the formation of mRNA upon transcription. In accordance with the present invention, the term „determining the expression level" preferably refers to the determination of the level of expression, namely of the markers.

Generally, "marker" refers to any genetically controlled difference which can be used in the genetic analysis of a test versus a control sample, for the purpose of assigning the sample to a defined genotype or phenotype. As used herein, "markers" refer to genes which are differentially expressed in, e.g., different AML subtypes. The markers can be defined by their gene symbol name, their encoded protein name, their transcript identification number (cluster identification number), the data base accession number, public accession number or GenBank identifier or, as done in the present invention, Affymetrix identification number, chromosomal location, UniGene accession number and cluster type, LocusLink accession number (see Examples and Tables).

The Affymetrix identification number (affy id) is accessible for anyone and the person skilled in the art by entering the "gene expression omnibus" internet page of the National Center for Biotechnology Information (NCBI) (http://www.ncbi.nlm.nih.gov/geo/). In particular, the affy id's of the

polynucleotides used for the method of the present invention are derived from the so-called U133 chip. The sequence data of each identification number can be viewed at http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL96

Generally, the expression level of a marker is determined by the determining the expression of its corresponding "polynucleotide" as described hereinafter.

According to the present invention, the term „polynucleotide" refers, generally, to a DNA, in particular cDNA, or RNA, in particular a cRNA, or a portion thereof or a polypeptide or a portion thereof. In the case of RNA (or cDNA), the polynucleotide is formed upon transcription of a nucleotide sequence which is capable of expression. The polynucleotide fragments refer to fragments preferably of between at least 8, such as 10, 12, 15 or 18 nucleotides and at least 50, such as 60, 80, 100, 200 or 300 nucleotides in length, or a complementary sequence thereto, representing a consecutive stretch of nucleotides of a gene, cDNA or mRNA. In other terms, polynucleotides include also any fragment (or complementary sequence thereto) of a sequence derived from any of the markers defined above as long as these fragments unambiguously identify the marker.

The determination of the expression level may be effected at the transcriptional or translational level, i.e. at the level of mRNA or at the protein level. Protein fragments such as peptides or polypeptides advantageously comprise between at least 6 and at least 25, such as 30, 40, 80, 100 or 200 consecutive amino acids representative of the corresponding full length protein. Six amino acids are generally recognized as the lowest peptidic stretch giving rise to a linear epitope recognized by an antibody, fragment or derivative thereof. Alternatively, the proteins or fragments thereof may be analysed using nucleic acid molecules specifically binding to three-dimensional structures (aptamers).

Depending on the nature of the polynucleotide or polypeptide, the determination of the expression levels may be effected by a variety of methods. For determining and detecting the expression level, it is preferred in the present invention that the polynucleotide, in particular the cRNA, is labelled.

The labelling of the polynucleotide or a polypeptide can occur by a variety of methods known to the skilled artisan. The label can be fluorescent, chemiluminescent, bioluminescent, radioactive (such as ^{3}H or ^{32}P). The labelling compound can be any labelling compound being suitable for the labelling of polynucleotides and/or polypeptides. Examples include fluorescent dyes, such as fluorescein, dichlorofluorescein, hexachlorofluorescein, BODIPY variants, ROX, tetramethylrhodamin, rhodamin X, Cyanine-2, Cyanine-3, Cyanine-5, Cyanine-7, IRD40, FluorX, Oregon Green, Alexa variants (available e.g. from Molecular Probes or Amersham Biosciences) and the like, biotin or biotinylated nucleotides, digoxigenin, radioisotopes, antibodies, enzymes and receptors. Depending on the type of labelling, the detection is done via fluorescence measurements, conjugation to streptavidin and/or avidin, antigen-antibody- and/or antibody-antibody-interactions, radioactivity measurements, as well as catalytic and/or receptor/ligand interactions. Suitable methods include the direct labelling (incorporation) method, the amino-modified (amino-allyl) nucleotide method (available e.g. from Ambion), and the primer tagging method (DNA dendrimer labelling, as kit available e.g. from Genisphere). Particularly preferred for the present invention is the use of biotin or biotinylated nucleotides for labelling, with the latter being directly incorporated into, e.g. the cRNA polynucleotide by in vitro transcription.

If the polynucleotide is mRNA, cDNA may be prepared into which a detectable label, as exemplified above, is incorporated. Said detectably labelled cDNA, in single-stranded form, may then be hybridised, preferably under stringent or highly stringent conditions to a panel of single-stranded oligonucleotides representing different genes and affixed to a solid support such as a chip. Upon applying appropriate washing steps, those cDNAs will be detected or quantitatively detected that have a counterpart in the oligonucleotide panel. Various advantageous embodiments of this general method are feasible. For example, the mRNA or the cDNA may be amplified e.g. by polymerase chain reaction, wherein it is preferable, for quantitative assessments, that the number of amplified copies corresponds relative to further amplified mRNAs or cDNAs to the number of mRNAs originally present in the cell. In a preferred embodiment of the present invention, the cDNAs are transcribed into cRNAs prior to the hybridisation step wherein only in the transcription step a label is incorporated into the nucleic acid and wherein the cRNA is employed for hybridisation. Alternatively, the label may be attached subsequent to the transcription step.

Similarly, proteins from a cell or tissue under investigation may be contacted with a panel of aptamers or of antibodies or fragments or derivatives thereof. The antibodies etc. may be affixed to a solid support such as a chip. Binding of proteins indicative of an AML subtype may be verified by binding to a detectably labelled secondary antibody or aptamer. For the labelling of antibodies, it is referred to Harlow and Lane, "Antibodies, a laboratory manual", CSH Press, 1988, Cold Spring Harbor. Specifically, a minimum set of proteins necessary for diagnosis of all AML subtypes may be selected for creation of a protein array system to make diagnosis on a protein lysate of a diagnostic bone marrow sample directly. Protein Array Systems for the detection of specific protein expression profiles already are available (for example: Bio-Plex, BIORAD, München, Germany). For this application preferably antibodies against the proteins have to be produced and immobilized on a platform e.g. glasslides or microtiterplates. The immobilized antibodies can be labelled with a reactant specific for the certain target proteins as discussed above. The reactants can include enzyme substrates, DNA, receptors, antigens or antibodies to create for example a capture sandwich immunoassay.

For reliably distinguishing AML subtypes it is useful that the expression of more than one of the above defined markers is determined. As a criterion for the choice of markers, the statistical significance of markers as expressed in q or p values based on the concept of the false discovery rate is determined. In doing so, a measure of statistical significance called the *q* value is associated with each tested feature. The *q* value is similar to the *p* value, except it is a measure of significance in terms of the false discovery rate rather than the false positive rate (Storey JD and Tibshirani R. Proc.Natl.Acad.Sci., 2003, Vol. 100:9440-5).

In a preferred embodiment of the present invention, markers as defined in Tables 1.1-2.21 having a q-value of less than 3E-06, more preferred less than 1.5E-09, most preferred less than 1.5E-11, less than 1.5E-20, less than 1.5E-30, are measured.

Of the above defined markers, the expression level of at least two, preferably of at least ten, more preferably of at least 25, most preferably of 50 of at least one of the Tables of the markers is determined.

In another preferred embodiment, the expression level of at least 2, of at least 5, of at least 10 out of the markers having the numbers 1 – 10, 1-20, 1-40, 1-50 of at least one of the Tables are measured.

The level of the expression of the „marker", i.e. the expression of the polynucleotide is indicative of the AML subtype of a cell or an organism. The level of expression of a marker or group of markers is measured and is compared with the level of expression of the same marker or the same group of markers from other cells or samples. The comparison may be effected in an actual experiment or in silico. When the expression level also referred to as expression pattern or expression signature (expression profile) is measurably different, there is according to the invention a meaningful difference in the level of expression. Preferably the difference at least is 5 %, 10% or 20%, more preferred at least 50% or may even be as high as 75% or 100%. More preferred the difference in the level of expression is at least 200%, i.e. two fold, at least 500%, i.e. five fold, or at least 1000%, i.e. 10 fold.

Accordingly, the expression level of markers expressed lower in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold lower, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold lower in the first subtype. On the other hand, the expression level of markers expressed higher in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold higher, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold higher in the first subtype.

In another embodiment of the present invention, the sample is derived from an individual having leukaemia, preferably AML.

For the method of the present invention it is preferred if the polynucleotide the expression level of which is determined is in form of a transcribed polynucleotide. A particularly preferred transcribed polynucleotide is an mRNA, a cDNA and/or a cRNA, with the latter being preferred. Transcribed polynucleotides are isolated from a sample, reverse transcribed and/or amplified, and labelled, by employing

methods well-known the person skilled in the art (see Example 3). In a preferred embodiment of the methods according to the invention, the step of determining the expression profile further comprises amplifying the transcribed polynucleotide.

In order to determine the expression level of the transcribed polynucleotide by the method of the present invention, it is preferred that the method comprises hybridizing the transcribed polynucleotide to a complementary polynucleotide, or a portion thereof, under stringent hybridization conditions, as described hereinafter.

The term "hybridizing" means hybridization under conventional hybridization conditions, preferably under stringent conditions as described, for example, in Sambrook, J., et al., in "Molecular Cloning: A Laboratory Manual" (1989), Eds. J. Sambrook, E. F. Fritsch and T. Maniatis, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, NY and the further definitions provided above. Such conditions are, for example, hybridization in 6x SSC, pH 7.0 / 0.1% SDS at about 45°C for 18-23 hours, followed by a washing step with 2x SSC/0.1% SDS at 50°C. In order to select the stringency, the salt concentration in the washing step can for example be chosen between 2x SSC/0.1% SDS at room temperature for low stringency and 0.2x SSC/0.1% SDS at 50°C for high stringency. In addition, the temperature of the washing step can be varied between room temperature, ca. 22°C, for low stringency, and 65°C to 70° C for high stringency. Also contemplated are polynucleotides that hybridize at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation, preferably of formamide concentration (lower percentages of formamide result in lowered stringency), salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH2PO4; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 mg/ml salmon sperm blocking DNA, followed by washes at 50°C with 1 X SSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5x SSC). Variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

"Complementary" and "complementarity", respectively, can be described by the percentage, i.e. proportion, of nucleotides which can form base pairs between two polynucleotide strands or within a specific region or domain of the two strands. Generally, complementary nucleotides are, according to the base pairing rules, adenine and thymine (or adenine and uracil), and cytosine and guanine. Complementarity may be partial, in which only some of the nucleic acids' bases are matched according to the base pairing rules. Or, there may be a complete or total complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has effects on the efficiency and strength of hybridization between nucleic acid strands.

Two nucleic acid strands are considered to be 100% complementary to each other over a defined length if in a defined region all adenines of a first strand can pair with a thymine (or an uracil) of a second strand, all guanines of a first strand can pair with a cytosine of a second strand, all thymine (or uracils) of a first strand can pair with an adenine of a second strand, and all cytosines of a first strand can pair with a guanine of a second strand, and vice versa. According to the present invention, the degree of complementarity is determined over a stretch of 20, preferably 25, nucleotides, i.e. a 60% complementarity means that within a region of 20 nucleotides of two nucleic acid strands 12 nucleotides of the first strand can base pair with 12 nucleotides of the second strand according to the above ruling, either as a stretch of 12 contiguous nucleotides or interspersed by non-pairing nucleotides, when the two strands are attached to each other over said region of 20 nucleotides. The degree of complementarity can range from at least about 50% to full, i.e. 100% complementarity. Two single nucleic acid strands are said to be "substantially complementary" when they are at least about 80% complementary, preferably about 90% or higher. For carrying out the method of the present invention substantial complementarity is preferred.

Preferred methods for detection and quantification of the amount of polynucleotides, i.e. for the methods according to the invention allowing the determination of the level of expression of a marker, are those described by Sambrook et al. (1989) or real time methods known in the art as the TaqMan® method disclosed in WO92/02638 and the corresponding U.S. 5,210,015, U.S. 5,804,375, U.S. 5,487,972. This method exploits the exonuclease activity of a polymerase to generate a signal. In detail, the (at least one) target nucleic acid

component is detected by a process comprising contacting the sample with an oligonucleotide containing a sequence complementary to a region of the target nucleic acid component and a labeled oligonucleotide containing a sequence complementary to a second region of the same target nucleic acid component sequence strand, but not including the nucleic acid sequence defined by the first oligonucleotide, to create a mixture of duplexes during hybridization conditions, wherein the duplexes comprise the target nucleic acid annealed to the first oligonucleotide and to the labeled oligonucleotide such that the 3'-end of the first oligonucleotide is adjacent to the 5'-end of the labeled oligonucleotide. Then this mixture is treated with a template-dependent nucleic acid polymerase having a 5' to 3' nuclease activity under conditions sufficient to permit the 5' to 3' nuclease activity of the polymerase to cleave the annealed, labeled oligonucleotide and release labeled fragments. The signal generated by the hydrolysis of the labeled oligonucleotide is detected and/ or measured. TaqMan® technology eliminates the need for a solid phase bound reaction complex to be formed and made detectable. Other methods include e.g. fluorescence resonance energy transfer between two adjacently hybridized probes as used in the LightCycler® format described in U.S. 6,174,670.

A preferred protocol if the marker, i.e. the polynucleotide, is in form of a transcribed nucleotide, is described in Example 3, where total RNA is isolated, cDNA and, subsequently, cRNA is synthesized and biotin is incorporated during the transcription reaction. The purified cRNA is applied to commercially available arrays which can be obtained e.g. from Affymetrix. The hybridized cRNA is detected according to the methods described in Example 3. The arrays are produced by photolithography or other methods known to experts skilled in the art e.g. from U.S. 5,445,934, U.S. 5,744,305, U.S. 5,700,637, U.S. 5,945,334 and EP 0 619 321 or EP 0 373 203, or as decribed hereinafter in greater detail.

In another embodiment of the present invention, the polynucleotide or at least one of the polynucleotides is in form of a polypeptide. In another preferred embodiment, the expression level of the polynucleotides or polypeptides is detected using a compound which specifically binds to the polynucleotide of the polypeptide of the present invention.

As used herein, "specifically binding" means that the compound is capable of discriminating between two or more polynucleotides or polypeptides, i.e. it binds to the desired polynucleotide or polypeptide, but essentially does not bind unspecifically to a different polynucleotide or polypeptide.

The compound can be an antibody, or a fragment thereof, an enzyme, a so-called small molecule compound, a protein-scaffold, preferably an anticalin. In a preferred embodiment, the compound specifically binding to the polynucleotide or polypeptide is an antibody, or a fragment thereof.

As used herein, an "antibody" comprises monoclonal antibodies as first described by Köhler and Milstein in Nature 278 (1975), 495-497 as well as polyclonal antibodies, i.e. antibodies contained in a polyclonal antiserum. Monoclonal antibodies include those produced by transgenic mice. Fragments of antibodies include $F(ab')_2$, Fab and Fv fragments. Derivatives of antibodies include scFvs, chimeric and humanized antibodies. See, for example Harlow and Lane, loc. cit. For the detection of polypeptides using antibodies or fragments thereof, the person skilled in the art is aware of a variety of methods, all of which are included in the present invention. Examples include immunoprecipitation, Western blotting, Enzyme-linked immuno sorbent assay (ELISA), Enzyme-linked immuno sorbent assay (RIA), dissociation-enhanced lanthanide fluoro immuno assay (DELFIA), scintillation proximity assay (SPA). For detection, it is desirable if the antibody is labelled by one of the labelling compounds and methods described supra.

In another preferred embodiment of the present invention, the method for distinguishing AML subtypes with different gene dosages selected from AML-TRI8, AML-TRI11, AML-TRI13, AML-MO7, and/or AML-DEL5q is carried out on an array.

In general, an "array" or "microarray" refers to a linear or two- or three dimensional arrangement of preferably discrete nucleic acid or polypeptide probes which comprises an intentionally created collection of nucleic acid or polypeptide probes of any length spotted onto a substrate/solid support. The person skilled in the art knows a collection of nucleic acids or polypeptide spotted onto a substrate/solid support also under the term "array". As known to the person skilled

in the art, a microarray usually refers to a miniaturised array arrangement, with the probes being attached to a density of at least about 10, 20, 50, 100 nucleic acid molecules referring to different or the same genes per cm^2. Furthermore, where appropriate an array can be referred to as "gene chip". The array itself can have different formats, e.g. libraries of soluble probes or libraries of probes tethered to resin beads, silica chips, or other solid supports.

The process of array fabrication is well-known to the person skilled in the art. In the following, the process for preparing a nucleic acid array is described. Commonly, the process comprises preparing a glass (or other) slide (e.g. chemical treatment of the glass to enhance binding of the nucleic acid probes to the glass surface), obtaining DNA sequences representing genes of a genome of interest, and spotting sequences these sequences of interest onto glass slide. Sequences of interest can be obtained via creating a cDNA library from an mRNA source or by using publicly available databases, such as GeneBank, to annotate the sequence information of custom cDNA libraries or to identify cDNA clones from previously prepared libraries. Generally, it is recommendable to amplify obtained sequences by PCR in order to have sufficient amounts of DNA to print on the array. The liquid containing the amplified probes can be deposited on the array by using a set of microspotting pins. Ideally, the amount deposited should be uniform. The process can further include UV-crosslinking in order to enhance immobilization of the probes on the array.

In a preferred embodiment, the array is a high density oligonucleotide (oligo) array using a light-directed chemical synthesis process, employing the so-called photolithography technology. Unlike common cDNA arrays, oligo arrays (according to the Affymetrix technology) use a single-dye technology. Given the sequence information of the markers, the sequence can be synthesized directly onto the array, thus, bypassing the need for physical intermediates, such as PCR products, required for making cDNA arrays. For this purpose, the marker, or partial sequences thereof, can be represented by 14 to 20 features, preferably by less than 14 features, more preferably less than 10 features, even more preferably by 6 features or less, with each feature being a short sequence of nucleotides (oligonucleotide), which is a perfect match (PM) to a segment of the respective gene. The PM oligonucleotide are paired with mismatch (MM) oligonucleotides which have a single mismatch at the central base of the nucleotide and are used as "controls". The chip exposure sites are defined by masks and are deprotected by

the use of light, followed by a chemical coupling step resulting in the synthesis of one nucleotide. The masking, light deprotection, and coupling process can then be repeated to synthesize the next nucleotide, until the nucleotide chain is of the specified length.

Advantageously, the method of the present invention is carried out in a robotics system including robotic plating and a robotic liquid transfer system, e.g. using microfluidics, i.e. channelled structured.

A particular preferred method according to the present invention is as follows:

1. Obtaining a sample, e.g. bone marrow or peripheral blood aliquots, from a patient having AML
2. Extracting RNA, preferably mRNA, from the sample
3. Reverse transcribing the RNA into cDNA
4. In vitro transcribing the cDNA into cRNA
5. Fragmenting the cRNA
6. Hybridizing the fragmented cRNA on standard microarrays
7. Determining hybridization

In another embodiment, the present invention is directed to the use of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, and/or 2 for the manufacturing of a diagnostic for distinguishing AML subtypes with different gene dosages selected from AML-TRI8, AML-TRI11, AML-TRI13, AML-MO7, and/or AML-DEL5q. The use of the present invention is particularly advantageous for distinguishing AML subtypes with different gene dosages selected from AML-TRI8, AML-TRI11, AML-TRI13, AML-MO7, and/or AML-DEL5q in an individual having AML. The use of said markers for diagnosis of AML subtypes with different gene dosages selected from AML-TRI8, AML-TRI11, AML-TRI13, AML-MO7, and/or AML-DEL5q, preferably based on microarray technology, offers the following advantages: (1) more rapid and more precise diagnosis, (2) easy to use in laboratories without specialized experience, (3) abolishes the requirement for analyzing viable cells for chromosome analysis (transport problem), and (4) very experienced hematologists for cytomorphology and cytochemistry, immunophenotyping as well as cytogeneticists and molecularbiologists are no longer required.

Accordingly, the present invention refers to a diagnostic kit containing at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, and/or 2 for distinguishing AML subtypes with different gene dosages selected from AML-TRI8, AML-TRI11, AML-TRI13, AML-MO7, and/or AML-DEL5q, in combination with suitable auxiliaries. Suitable auxiliaries, as used herein, include buffers, enzymes, labelling compounds, and the like. In a preferred embodiment, the marker contained in the kit is a nucleic acid molecule which is capable of hybridizing to the mRNA corresponding to at least one marker of the present invention. Preferably, the at least one nucleic acid molecule is attached to a solid support, e.g. a polystyrene microtiter dish, nitrocellulose membrane, glass surface or to non-immobilized particles in solution.

In another preferred embodiment, the diagnostic kit contains at least one reference for an AML subtype with different gene dosages selected from AML-TRI8, AML-TRI11, AML-TRI13, AML-MO7, and/or AML-DEL5q. As used herein, the reference can be a sample or a data bank.

In another embodiment, the present invention is directed to an apparatus for distinguishing AML subtypes with different gene dosages selected from AML-TRI8, AML-TRI11, AML-TRI13, AML-MO7, and/or AML-DEL5q in a sample, containing a reference data bank obtainable by comprising

(a) compiling a gene expression profile of a patient sample by determining the expression level at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, and/or 2, and

(b) classifying the gene expression profile by means of a machine learning algorithm.

According to the present invention, the "machine learning algorithm" is a computational-based prediction methodology, also known to the person skilled in the art as "classifier", employed for characterizing a gene expression profile. The signals corresponding to a certain expression level which are obtained by the microarray hybridization are subjected to the algorithm in order to classify the expression profile. Supervised learning involves "training" a classifier to recognize the distinctions among classes and then "testing" the accuracy of the classifier on

an independent test set. For new, unknown samples the classifier shall predict into which class the sample belongs.

Preferably, the machine learning algorithm is selected from the group consisting of Weighted Voting, K-Nearest Neighbors, Decision Tree Induction, Support Vector Machines (SVM), and Feed-Forward Neural Networks. Most preferably, the machine learning algorithm is Support Vector Machine, such as polynomial kernel and Gaussian Radial Basis Function-kernel SVM models.

The classification accuracy of a given gene list for a set of microarray experiments is preferably estimated using Support Vector Machines (SVM), because there is evidence that SVM-based prediction slightly outperforms other classification techniques like k-Nearest Neighbors (k-NN). The LIBSVM software package version 2.36 was used (SVM-type: C-SVC, linear kernel (http://www.csie.ntu.edu.tw/~cjlin/libsvm/)). The skilled artisan is furthermore referred to Brown et al., Proc.Natl.Acad.Sci., 2000; 97: 262-267, Furey et al., Bioinformatics. 2000; 16: 906-914, and Vapnik V. Statistical Learning Theory. New York: Wiley, 1998.

In detail, the classification accuracy of a given gene list for a set of microarray experiments can be estimated using Support Vector Machines (SVM) as supervised learning technique. Generally, SVMs are trained using differentially expressed genes which were identified on a subset of the data and then this trained model is employed to assign new samples to those trained groups from a second and different data set. Differentially expressed genes were identified applying ANOVA and t-test-statistics (Welch t-test). Based on identified distinct gene expression signatures respective training sets consisting of 2/3 of cases and test sets with 1/3 of cases to assess classification accuracies are designated. Assignment of cases to training and test set is randomized and balanced by diagnosis. Based on the training set a Support Vector Machine (SVM) model is built.

According to the present invention, the apparent accuracy, i.e. the overall rate of correct predictions of the complete data set was estimated by 10fold cross validation. This means that the data set was divided into 10 approximately equally sized subsets, an SVM-model was trained for 9 subsets and predictions were

generated for the remaining subset. This training and prediction process was repeated 10 times to include predictions for each subset. Subsequently the data set was split into a training set, consisting of two thirds of the samples, and a test set with the remaining one third. Apparent accuracy for the training set was estimated by 10fold cross validation (analogous to apparent accuracy for complete set). A SVM-model of the training set was built to predict diagnosis in the independent test set, thereby estimating true accuracy of the prediction model. This prediction approach was applied both for overall classification (multi-class) and binary classification (diagnosis X => yes or no). For the latter, sensitivity and specificity were calculated:

Sensitivity = (number of positive samples predicted)/(number of true positives)

Specificity = (number of negative samples predicted)/(number of true negatives)

In a preferred embodiment, the reference data bank is backed up on a computational data memory chip which can be inserted in as well as removed from the apparatus of the present invention, e.g. like an interchangeable module, in order to use another data memory chip containing a different reference data bank.

The apparatus of the present invention containing a desired reference data bank can be used in a way such that an unknown sample is, first, subjected to gene expression profiling, e.g. by microarray analysis in a manner as described supra or in the art, and the expression level data obtained by the analysis are, second, fed into the apparatus and compared with the data of the reference data bank obtainable by the above method. For this purpose, the apparatus suitably contains a device for entering the expression level of the data, for example a control panel such as a keyboard. The results, whether and how the data of the unknown sample fit into the reference data bank can be made visible on a provided monitor or display screen and, if desired, printed out on an incorporated of connected printer.

Alternatively, the apparatus of the present invention is equipped with particular appliances suitable for detecting and measuring the expression profile data and, subsequently, proceeding with the comparison with the reference data bank. In this embodiment, the apparatus of the present invention can contain a gripper arm and/or a tray which takes up the microarray containing the hybridized nucleic acids.

In another embodiment, the present invention refers to a reference data bank for distinguishing AML subtypes with different gene dosages selected from AML-TRI8, AML-TRI11, AML-TRI13, AML-MO7, and/or AML-DEL5q in a sample obtainable by comprising

(a) compiling a gene expression profile of a patient sample by determining the expression level of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, and/or 2, and

(b) classifying the gene expression profile by means of a machine learning algorithm.

Preferably, the reference data bank is backed up and/or contained in a computational memory data chip.

The invention is further illustrated in the following table and examples, without limiting the scope of the invention:

TABLES 1.1-2.21

Tables 1.1-2.21 show AML subtype analysis of AML subtypes with different gene dosages selected from AML-TRI8, AML-TRI11, AML-TRI13, AML-MO7, and/or AML-DEL5q. The analysed markers are ordered according to their q-values, beginning with the lowest q-values.

For convenience and a better understanding, Tables 1.1 to 2.78 are accompanied with explanatory tables (Table 1.1A to 2.21A) where the numbering and the Affymetrix Id are further defined by other parameters, e.g. gene bank accession number.

EXAMPLES

Example 1: General experimental design of the invention and results

Acute myeloid leukemia (AML) is a heterogeneous group of diseases. From a genetic point of view 3 subgroups can be distinguished: 1. AML with normal karyotype, 2. AML with balanced chromosome aberrations, and 3. AML with unbalanced karyotype abnormalities characterized by gains and/or losses usually of

larger regions of the genome. The important pathogenetic role of leukemia specific fusion transcripts has been proven. The role of gains and losses of parts of the genome in AML with unbalanced karyotype is less clear. It has been assumed that gene dosage effects may play an important role in the pathogenesis of this AML subgroup. Virtaneva et al. supported this hypothesis showing that AML with trisomy 8 as the sole karyotype abnormality overexpressed genes located on chromosome 8 compared to AML with normal karyotype (PNAS, 2001). It was the aim of this study to investigate whether gains and losses on the genomic level translate into altered expression also in other areas of the genome. Therefore, we performed gene expression analysis using oligonucleotide microarrays covering 33,000 transcripts (Affymetrix U133 set) in AML cases with one of the following karyotype abnormalities as the sole change: +8 (AML-TRI8, n=12), +11 (AML-TRI11, n=7), +13 (AML-TRI13, n=7), -7 (AML-MO7, n=9), and del(5q) (AML-DEL5q, n=7). Gene expression data were compared to 104 AML with normal karyotype (AML-NK). For each gene/probe set 1) mean expression values were calculated within each group and 2) ratios between groups were determined. The median ratio of genes on chromosome 8 between AML-TRI8 cases and AML-NK was 1.27 confirming a gene dosage effect as published. For genes located on chromosome 11 the median ratio of AML-TRI11 and AML-NK was 1.25, for genes on chromosome 13 between AML-TRI13 and AML-NK the respective value was 1.14. Comparing the expression of genes located on chromosome 7 between AML-MO7 and AML-NK revealed a median ratio of 0.57, for genes located on 5q13 to 5q31 the respective value for AML-DEL5q vs AML-NK was 0.82. To identify differentially expressed genes we applied ANOVA and t-test-statistics (Welch t-test). The top 50 differentially expressed probe sets for each subtype vs all other subtypes were evaluated. The top 50 genes were equally distributed over the genome for each of the comparisons AML-TRI8, AML-TRI11, AML-TRI13 vs all other subtypes. Comparing AML-DEL5q with all other subtypes revealed that 10 of the 34 probe sets for which chromosomal location was available are located on chromosome 5 within the region affected by the deletion. These represent 8 genes involved in signal transduction (HINT1, PDE8B, SNX2, CSNK1A1, ANXA6), suppression of invasion (CTNNA1), and radioadaptive response (HSPA4), respectively. For 43 of the top 50 probe sets differentially expressed between AML-MO7 and all other subtypes chromosomal location is known. Of these 43 probesets 39 representing 36 different genes are localized on chromosome 7. They are involved in mismatch repair (PMS2L1, PMS2L3, PMS2L5, PMS2L8, PMS2L9), apoptosis (TAX1BP1, CASP2, CARD4), DNA replication (RIP60,

SSBP1), and signal transduction (AKAP9, CARD4). Also HOXA3 and HOXA9 were significantly lower expressed in AML-MO7 compared to all other subtypes. In conclusion, gain of whole chromosomes leads to overexpression of genes located on the respective chromosomes. Losses of larger regions of the genome translate into lower expression of the majority of genes represented by only one allele. The reduced expression of these genes is the most characteristic difference in gene expression between AML-MO7 and AML-DEL5Q and other AML subtypes. Therefore, these data provide evidence that gene dosage effects play an important role in AML with unbalanced karyotype abnormalities.

Example 2: General materials, methods and definitions of functional annotations

The methods section contains both information on statistical analyses used for identification of differentially expressed genes and detailed annotation data of identified microarray probesets.

Affymetrix Probeset Annotation

All annotation data of GeneChip® arrays are extracted from the NetAffx™ Analysis Center (internet website: www.affymetrix.com). Files for U133 set arrays, including U133A and U133B microarrays are derived from the June 2003 release. The original publication refers to: Liu G, Loraine AE, Shigeta R, Cline M, Cheng J, Valmeekam V, Sun S, Kulp D, Siani-Rose MA. NetAffx: Affymetrix probesets and annotations. Nucleic Acids Res. 2003;31(1):82-6.

The sequence data are omitted due to their large size, and because they do not change, whereas the annotation data are updated periodically, for example new information on chromomal location and functional annotation of the respective gene products. Sequence data are available for download in the NetAffx Download Center (www.affymetrix.com)

Data fields:

In the following section, the content of each field of the data files are described. Microarray probesets, for example found to be differentially expressed between different types of leukemia samples are further described by additional information. The fields are of the following types:

1. GeneChip Array Information
2. Probe Design Information
3. Public Domain and Genomic References

1. GeneChip Array Information

HG-U133 ProbeSet_ID:
HG-U133 ProbeSet_ID describes the probe set identifier. Examples are: 200007_at, 200011_s_at, 200012_x_at.

GeneChip:
The description of the GeneChip probe array name where the respective probeset is represented. Examples are: Affymetrix Human Genome U133A Array or Affymetrix Human Genome U133B Array.

2. Probe Design Information

Sequence Type:
The Sequence Type indicates whether the sequence is an Exemplar, Consensus or Control sequence. An Exemplar is a single nucleotide sequence taken directly from a public database. This sequence could be an mRNA or EST. A Consensus sequence, is a nucleotide sequence assembled by Affymetrix, based on one or more sequence taken from a public database.

Transcript ID:
The cluster identification number with a sub-cluster identifier appended.

Sequence Derived From:
The accession number of the single sequence, or representative sequence on which the probe set is based. Refer to the "Sequence Source" field to determine the database used.

Sequence ID:
For Exemplar sequences: Public accession number or GenBank identifier. For Consensus sequences: Affymetrix identification number or public accession number.

Sequence Source:
The database from which the sequence used to design this probe set was taken. Examples are: GenBank®, RefSeq, UniGene, TIGR (annotations from The Institute for Genomic Research).

3. Public Domain and Genomic References

Most of the data in this section come from LocusLink and UniGene databases, and are annotations of the reference sequence on which the probe set is modeled.

Gene Symbol and Title:
A gene symbol and a short title, when one is available. Such symbols are assigned by different organizations for different species. Affymetrix annotational data come from the UniGene record. There is no indication which species-specific databank was used, but some of the possibilities include for example HUGO: The Human Genome Organization.

MapLocation:
The map location describes the chromosomal location when one is available.

Unigene_Accession:
UniGene accession number and cluster type. Cluster type can be "full length" or "est", or "---" if unknown.

LocusLink:
This information represents the LocusLink accession number.

Full Length Ref. Sequences:
Indicates the references to multiple sequences in RefSeq. The field contains the ID and description for each entry, and there can be multiple entries per probeSet.

Example 3: Sample preparation, processing and data analysis

Method 1:

Microarray analyses were performed utilizing the GeneChip® System (Affymetrix, Santa Clara, USA). Hybridization target preparations were performed according to recommended protocols (Affymetrix Technical Manual). In detail, at time of diagnosis, mononuclear cells were purified by Ficoll-Hypaque density centrifugation. They had been lysed immediately in RLT buffer (Qiagen, Hilden, Germany), frozen, and stored at -80°C from 1 week to 38 months. For gene expression profiling cell lysates of the leukemia samples were thawed, homogenized (QIAshredder, Qiagen), and total RNA was extracted (RNeasy Mini Kit, Qiagen). Subsequently, 5-10 µg total RNA isolated from 1 x 10^7 cells was used as starting material for cDNA synthesis with oligo[$(dT)_{24}$T7promotor]$_{65}$ primer (cDNA Synthesis System, Roche Applied Science, Mannheim, Germany). cDNA products were purified by phenol/chlorophorm/IAA extraction (Ambion, Austin, USA) and acetate/ethanol-precipitated overnight. For detection of the hybridized target nucleic acid biotin-labeled ribonucleotides were incorporated during the following *in vitro* transcription reaction (Enzo BioArray HighYield RNA Transcript Labeling Kit, Enzo Diagnostics). After quantification by spectrophotometric measurements and 260/280 absorbance values assessment for quality control of the purified cRNA (RNeasy Mini Kit, Qiagen), 15 µg cRNA was fragmented by alkaline treatment (200 mM Tris-acetate, pH 8.2/500 mM potassium acetate/150 mM magnesium acetate) and added to the hybridization cocktail sufficient for five hybridizations on standard GeneChip microarrays (300 µl final volume). Washing and staining of the probe arrays was performed according to the recommended Fluidics Station protocol (EukGE-WS2v4). Affymetrix Microarray Suite software (version 5.0.1) extracted fluorescence signal intensities from each feature on the microarrays as detected by confocal laser scanning according to the manufacturer's recommendations.

Expression analysis quality assessment parameters included visiual array inspection of the scanned image for the presence of image artifacts and correct grid alignment for the identification of distinct probe cells as well as both low 3'/5' ratio of housekeeping controls (mean: 1.90 for GAPDH) and high percentage of detection calls (mean: 46.3% present called genes). The 3' to 5' ratio of GAPDH probesets can be used to assess RNA sample and assay quality. Signal values of the

3' probe sets for GAPDH are compared to the Signal values of the corresponding 5' probe set. The ratio of the 3' probe set to the 5' probe set is generally no more than 3.0. A high 3' to 5' ratio may indicate degraded RNA or inefficient synthesis of ds cDNA or biotinylated cRNA (GeneChip® Expression Analysis Technical Manual, www.affymetrix.com). Detection calls are used to determine whether the transcript of a gene is detected (present) or undetected (absent) and were calculated using default parameters of the Microarray Analysis Suite MAS 5.0 software package.

Method 2:

Bone marrow (BM) aspirates are taken at the time of the initial diagnostic biopsy and remaining material is immediately lysed in RLT buffer (Qiagen), frozen and stored at -80 C until preparation for gene expression analysis. For microarray analysis the GeneChip System (Affymetrix, Santa Clara, CA, USA) is used. The targets for GeneChip analysis are prepared according to the current Expression Analysis. Briefly, frozen lysates of the leukemia samples are thawed, homogenized (QIAshredder, Qiagen) and total RNA extracted (RNeasy Mini Kit, Qiagen).Normally 10 ug total RNA isolated from 1 x 107 cells is used as starting material in the subsequent cDNA-Synthesis using Oligo-dT-T7-Promotor Primer (cDNA synthesis Kit, Roche Molecular Biochemicals). The cDNA is purified by phenol-chlorophorm extraction and precipitated with 100% Ethanol over night. For detection of the hybridized target nucleic acid biotin-labeled ribonucleotides are incorporated during the in vitro transcription reaction (Enzo® BioArray™ HighYield™ RNA Transcript Labeling Kit, ENZO). After quantification of the purified cRNA (RNeasy Mini Kit, Qiagen), 15 ug are fragmented by alkaline treatment (200 mM Tris-acetate, pH 8.2, 500 mM potassium acetate, 150 mM magnesium acetate) and added to the hybridization cocktail sufficient for 5 hybridizations on standard GeneChip microarrays. Before expression profiling Test3 Probe Arrays (Affymetrix) are chosen for monitoring of the integrity of the cRNA. Only labeled cRNA-cocktails which showed a ratio of the messured intensity of the 3' to the 5' end of the GAPDH gene less than 3.0 are selected for subsequent hybridization on HG-U133 probe arrays (Affymetrix). Washing and staining the Probe arrays is performed as described (siehe Affymetrix-Original-Literatur (LOCKHART und LIPSHUTZ). The Affymetrix software (Microarray Suite, Version 4.0.1) extracted fluorescence intensities from each element on the

arrays as detected by confocal laser scanning according to the manufacturers recommendations.

Table 1

1. One-Versus-All (OVA)

1.1	AML_+11 versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	205055_at	ITGAE	-2.13	1.53E-10	2.55E-08	-1.16	-11.88	17p13
2	230322_at	NFAM1	-2.82	8.23E-16	1.31E-12	-1.03	-11.82	22q13.2
3	221002_s_at	DC-TM4F2	-2.09	3.99E-20	4.46E-16	-0.96	-11.63	10q22.3
4	229168_at	DKFZp434K0621	-2.79	6.45E-20	4.81E-16	-0.90	-11.01	5q35.3
5	210042_s_at	CTSZ	-3.31	2.11E-18	7.87E-15	-0.90	-10.87	20q13
6	214835_s_at	SUCLG2	-6.10	2.31E-09	2.33E-07	-1.09	-10.86	3p14.2
7	200923_at	LGALS3BP	-9.91	1.93E-20	4.31E-16	-0.87	-10.80	17q25
8	212459_x_at	SUCLG2	-5.50	1.37E-08	9.47E-07	-1.09	-10.54	3p14.2
9	225065_x_at	MGC40157	-2.70	1.05E-11	2.81E-09	-0.96	-10.51	17p11.2
10	242574_at	KIAA0674	-4.13	1.97E-18	7.87E-15	-0.85	-10.38	9q32
11	238730_at	ARHGEF11	-3.59	1.50E-13	9.86E-11	-0.90	-10.35	1q21
12	242345_at		-4.70	1.54E-18	7.87E-15	-0.84	-10.34	
13	217528_at	CLCA2	-4.80	8.15E-18	2.28E-14	-0.83	-10.21	1p31-p22
14	230495_at	LOC150568	-4.61	5.52E-18	1.76E-14	-0.83	-10.20	2q12.1
15	224132_at	MGC13008	-1.66	3.59E-09	3.25E-07	-0.99	-10.03	17p11.2
16	228519_x_at	CIRBP	-1.62	1.39E-09	1.55E-07	-0.97	-10.02	19p13.3
17	219085_s_at	GEMIN7	-3.35	5.66E-11	1.18E-08	-0.91	-9.94	19q13.32
18	242767_at		-2.72	9.61E-13	4.08E-10	-0.87	-9.92	
19	208438_s_at	FGR	-5.13	4.73E-17	1.17E-13	-0.81	-9.90	1p36.2-p36.1
20	215772_x_at	SUCLG2	-5.21	4.22E-08	2.31E-06	-1.03	-9.89	3p14.2
21	235749_at	UGCGL2	-5.52	1.31E-12	5.06E-10	-0.87	-9.86	13q32.1
22	210248_at	WNT7A	-3.17	3.23E-15	4.51E-12	-0.83	-9.85	3p25
23	218389_s_at	APH-1A	-1.81	3.47E-09	3.17E-07	-0.96	-9.84	1p36.13-q31.3
24	223794_at	DKFZP434P1735	-3.96	3.59E-14	3.34E-11	-0.83	-9.73	10p12.1
25	216548_x_at		-2.66	1.94E-07	8.27E-06	-1.06	-9.73	
26	219505_at	CECR1	-5.24	2.35E-16	5.26E-13	-0.78	-9.58	22q11.2
27	227750_at	TRAD	-1.81	9.80E-15	1.04E-11	-0.80	-9.56	3q21.2
28	243230_at		-4.73	4.49E-15	5.91E-12	-0.77	-9.31	
29	238209_at		-2.94	6.11E-13	2.85E-10	-0.80	-9.29	
30	235842_at		-3.60	1.24E-11	3.21E-09	-0.82	-9.26	
31	217168_s_at	HERPUD1	-2.35	9.42E-09	7.02E-07	-0.90	-9.25	16q12.2-q13
32	209706_at	NKX3-1	-2.26	1.37E-10	2.36E-08	-0.84	-9.24	8p21
33	223861_at	DKFZP434A1315	-4.00	6.21E-12	1.80E-09	-0.81	-9.22	1q21.2
34	231514_at	MGC15882	-2.18	6.87E-15	7.68E-12	-0.76	-9.21	1p34.3
35	222134_at	DDO	-5.55	3.29E-16	6.69E-13	-0.74	-9.17	6q21
36	232464_at	TRIMP1	-1.67	3.71E-12	1.17E-09	-0.80	-9.17	11p15
37	241234_at		-1.83	3.24E-10	4.93E-08	-0.84	-9.16	
38	203798_s_at	VSNL1	-4.21	1.20E-15	1.79E-12	-0.74	-9.11	2p24.3
39	216413_at		-4.27	6.11E-16	1.14E-12	-0.73	-9.05	
40	228367_at	HAK	-1.74	1.16E-12	4.63E-10	-0.77	-9.03	18q21.31

Table 1+2

41	207430_s_at	MSMB	-4.55	7.16E-16	1.23E-12	-0.73	-9.02	10q11.2
42	233705_at		-2.24	1.64E-12	6.11E-10	-0.77	-9.02	
43	239023_at	AF1Q	-2.63	4.69E-14	4.03E-11	-0.75	-8.98	1q21
44	232340_at		-1.69	1.34E-08	9.35E-07	-0.87	-8.93	
45	221841_s_at		-5.36	1.25E-09	1.43E-07	-0.83	-8.92	
46	242718_at		-2.69	2.95E-11	6.81E-09	-0.78	-8.90	
47	226129_at		-2.24	6.35E-12	1.82E-09	-0.77	-8.88	
48	218660_at	DYSF	-4.56	2.18E-09	2.21E-07	-0.83	-8.88	2p13.3-p13.1
49	209696_at	FBP1	-5.91	5.81E-15	6.84E-12	-0.72	-8.85	9q22.3
50	219071_x_at	LOC51236	-1.52	1.43E-07	6.42E-06	-0.90	-8.77	8q24.3
1.2	AML_+13 versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203955_at	KIAA0649	-9.26	7.05E-15	4.79E-12	-1.48	-15.80	9q34.3
2	224839_s_at	GPT2	-11.55	1.10E-30	2.89E-26	-1.21	-14.96	16q12.1
3	233255_s_at	BIVM	-18.14	1.77E-30	2.89E-26	-1.21	-14.95	13q32-q33.1
4	203949_at	MPO	-12.26	9.48E-29	1.03E-24	-1.18	-14.54	17q23.1
5	217963_s_at	NGFRAP1	-10.78	1.77E-21	7.22E-18	-1.14	-13.57	Xq22.1
6	212688_at	PIK3CB	-3.05	9.02E-17	9.50E-14	-1.19	-13.45	3q22.3
7	230206_at		-9.95	9.90E-12	3.23E-09	-1.26	-13.06	
8	226141_at		-6.06	9.32E-26	7.60E-22	-1.03	-12.85	
9	209267_s_at	BIGM103	-3.41	9.99E-16	8.14E-13	-1.12	-12.66	4q22-q24
10	203948_s_at	MPO	-17.61	3.08E-25	2.01E-21	-1.01	-12.57	17q23.1
11	239598_s_at	FLJ20481	-4.96	2.29E-12	9.18E-10	-1.15	-12.31	16q12.1
12	222668_at	MGC2628	-7.10	3.51E-15	2.60E-12	-1.08	-12.25	19q13.11
13	220773_s_at	GPHN	-6.84	2.66E-12	1.02E-09	-1.15	-12.24	14q23.3
14	220416_at	KIAA1939	-5.99	3.49E-18	4.56E-15	-1.04	-12.23	15q15.3
15	226763_at	DKFZp434O0515	-4.56	9.07E-12	3.02E-09	-1.16	-12.18	2q31.3
16	217975_at	LOC51186	-5.65	5.39E-16	4.62E-13	-1.06	-12.14	Xq22.1
17	227001_at		-3.61	7.06E-12	2.45E-09	-1.13	-12.00	
18	205653_at	CTSG	-12.28	1.96E-22	1.06E-18	-0.95	-11.75	14q11.2
19	238784_at	FLJ32949	-7.29	1.65E-21	7.22E-18	-0.95	-11.70	12q14.1
20	208626_s_at	VAT1	-2.49	8.40E-12	2.83E-09	-1.08	-11.57	17q21
21	238021_s_at		-9.71	5.85E-21	1.47E-17	-0.95	-11.56	
22	222664_at	MGC2628	-5.08	1.48E-10	3.43E-08	-1.11	-11.43	19q13.11
23	242476_at		-3.11	1.23E-14	7.31E-12	-1.00	-11.40	
24	230207_s_at		-3.79	9.37E-10	1.66E-07	-1.13	-11.34	
25	209619_at	CD74	1.68	1.50E-09	2.45E-07	1.12	11.19	5q32
26	213110_s_at	COL4A5	-10.42	2.76E-21	7.53E-18	-0.90	-11.17	Xq22
27	232424_at	PRDM16	-25.11	2.15E-21	7.53E-18	-0.91	-11.17	1p36.23-p33
28	209739_s_at	DXS1283E	-5.58	2.77E-21	7.53E-18	-0.90	-11.16	Xp22.3
29	229838_at	NUCB2	-2.49	5.91E-10	1.10E-07	-1.10	-11.15	11p15.1-p14
30	212686_at	KIAA1157	-4.31	9.77E-12	3.22E-09	-1.03	-11.13	12q13.3
31	242269_at	DKFZp761G0122	-3.49	2.37E-21	7.53E-18	-0.90	-11.13	1p36.32

32	213844_at	HOXA5	-7.20	3.84E-13	1.76E-10	-0.99	-11.08	7p15-p14
33	219869_s_at	BIGM103	-3.16	1.58E-11	4.86E-09	-1.03	-11.06	4q22-q24
34	206480_at	LTC4S	-7.61	7.46E-21	1.74E-17	-0.89	-11.04	5q35
35	219078_at	FLJ10252	-2.56	1.30E-10	3.09E-08	-1.05	-10.98	1q41
36	204306_s_at	CD151	-5.22	5.29E-19	9.59E-16	-0.90	-10.97	11p15.5
37	223703_at	CDA017	-4.05	1.06E-09	1.84E-07	-1.08	-10.95	10q23.1
38	214575_s_at	AZU1	-11.98	1.04E-16	1.06E-13	-0.91	-10.85	19p13.3
39	209099_x_at	JAG1	-9.87	2.17E-18	2.95E-15	-0.89	-10.82	20p12.1-p11.23
40	219479_at	KDELC1	-15.08	5.08E-20	1.10E-16	-0.87	-10.80	13q33
41	238022_at		-8.37	4.75E-19	9.12E-16	-0.87	-10.66	
42	230263_s_at		-4.28	1.49E-07	1.40E-05	-1.18	-10.57	
43	223319_at	GPHN	-15.23	7.82E-20	1.59E-16	-0.85	-10.54	14q23.3
44	208654_s_at	CD164	-1.76	1.69E-11	5.16E-09	-0.97	-10.52	6q21
45	212173_at	AK2	-3.14	8.94E-11	2.25E-08	-0.98	-10.49	1p34
46	216268_s_at	JAG1	-9.38	3.32E-16	3.09E-13	-0.87	-10.42	20p12.1-p11.23
47	201952_at	ALCAM	-2.70	1.89E-11	5.71E-09	-0.95	-10.33	3q13.1
48	227889_at		-6.68	1.19E-09	2.02E-07	-1.00	-10.31	
49	235391_at	LOC137392	-4.96	8.93E-19	1.40E-15	-0.83	-10.28	8q21.3
50	216920_s_at	TRGV9	-4.35	4.84E-12	1.74E-09	-0.92	-10.26	7p15
1.3	AML_+8 versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	200923_at	LGALS3BP	-6.51	5.83E-16	2.10E-11	-0.75	-9.25	17q25
2	225406_at	TWSG1	-2.14	7.56E-09	1.87E-05	-0.84	-8.35	18p11.3
3	206761_at	TACTILE	-7.43	6.03E-14	9.42E-10	-0.66	-8.27	3q13.13
4	212489_at	COL5A1	-4.76	7.83E-14	9.42E-10	-0.66	-8.24	9q34.2-q34.3
5	243579_at	MSI2	-4.05	2.75E-11	2.48E-07	-0.71	-8.18	17q23.1
6	213110_s_at	COL4A5	-4.08	3.58E-11	2.58E-07	-0.67	-7.81	Xq22
7	225889_at	MGC17922	-1.72	1.33E-08	2.52E-05	-0.74	-7.64	12p12.3
8	211907_s_at	PARD6B	-2.62	4.31E-11	2.59E-07	-0.60	-7.31	20q13.13
9	212259_s_at	HPIP	-3.41	6.58E-11	3.39E-07	-0.60	-7.28	1q21.3
10	225102_at	LOC152009	-2.23	8.38E-08	8.89E-05	-0.70	-7.12	3q21.3
11	235124_at		-1.70	1.42E-08	2.55E-05	-0.64	-7.00	
12	204116_at	IL2RG	-2.23	4.84E-09	1.34E-05	-0.62	-7.00	Xq13.1
13	225238_at		-3.33	1.69E-09	5.56E-06	-0.59	-6.91	
14	215071_s_at	HIST1H2AC	-2.88	7.76E-09	1.87E-05	-0.61	-6.90	6p21.3
15	231903_x_at	KIAA1501	-2.48	1.65E-09	5.56E-06	-0.59	-6.89	17q21.1
16	225240_s_at		-2.89	5.17E-08	6.22E-05	-0.65	-6.89	
17	226807_at	FLJ34243	-1.83	1.52E-07	0.00013387	-0.67	-6.86	16q22.3
18	228654_at	LOC139886	-2.02	2.84E-07	0.0001968	-0.68	-6.78	Xq11.1
19	220240_s_at	C13orf11	-1.89	3.03E-07	0.00020642	-0.68	-6.77	13q34
20	243010_at	MSI2	-2.16	1.03E-08	2.23E-05	-0.57	-6.59	17q23.1
21	219663_s_at	MGC4659	-2.70	2.90E-09	8.72E-06	-0.54	-6.52	14q32.33
22	205910_s_at	CEL	-3.53	1.02E-09	4.62E-06	-0.52	-6.51	9q34.3

23	233040_at		-5.04	1.16E-09	4.64E-06	-0.52	-6.49	
24	216412_x_at	IGL	-2.82	1.71E-08	2.94E-05	-0.56	-6.45	22q11.1-q11.2
25	219553_at	NME7	-1.66	1.08E-08	2.23E-05	-0.55	-6.44	1q24
26	208457_at	GABRD	-2.23	3.40E-08	4.91E-05	-0.57	-6.42	1p36.3
27	214029_at		-2.69	3.34E-08	4.91E-05	-0.55	-6.35	
28	229174_at	MGC26717	-1.57	1.22E-06	0.00062746	-0.65	-6.35	3q11.1
29	220591_s_at	FLJ22843	-1.82	5.75E-07	0.00037062	-0.62	-6.35	Xp11.3
30	214436_at	FBXL2	-2.04	2.51E-08	3.94E-05	-0.54	-6.32	3p22.2
31	218731_s_at	FLJ22215	-2.48	1.23E-07	0.00011881	-0.55	-6.18	1p36.33
32	222490_at	RPC5	-1.88	5.09E-06	0.0015814	-0.68	-6.18	16p12.3
33	225073_at	PPHLN1	-1.41	2.87E-06	0.00105411	-0.64	-6.16	12q12
34	228907_at		-3.23	1.11E-08	2.23E-05	-0.50	-6.15	
35	216554_s_at	ENO1	-1.34	9.96E-07	0.0005529	-0.60	-6.14	1p36.3-p36.2
36	237216_at		-3.24	4.10E-08	5.28E-05	-0.52	-6.11	
37	238935_at	RPS27L	-1.72	7.96E-07	0.00045554	-0.58	-6.09	15q21.3
38	206049_at	SELP	-1.83	8.82E-08	9.09E-05	-0.53	-6.08	1q22-q25
39	218999_at	FLJ11000	-1.79	2.45E-07	0.00017551	-0.55	-6.08	7q33
40	211743_s_at	PRG2	-5.45	3.84E-08	5.28E-05	-0.51	-6.05	11q12
41	214177_s_at	HPIP	-1.68	2.75E-06	0.00105411	-0.62	-6.05	1q21.3
42	220885_s_at	CENPJ	-1.53	1.54E-06	0.00072179	-0.59	-6.02	13q12.12
43	228092_at	CREM	-1.65	8.13E-06	0.00216777	-0.67	-6.01	10p12.1-p11.1
44	204468_s_at	TIE	-6.08	4.96E-08	6.16E-05	-0.50	-5.98	1p34-p33
45	209618_at	CTNND2	-1.97	4.00E-08	5.28E-05	-0.50	-5.97	5p15.2
46	219776_s_at	FLJ11125	-2.20	1.02E-06	0.00055473	-0.57	-5.97	8p21.2
47	212250_at		1.40	3.82E-05	0.00669525	0.84	5.96	
48	227943_at		-2.04	1.33E-07	0.00012263	-0.52	-5.96	
49	225237_s_at		-2.46	2.29E-06	0.00094826	-0.59	-5.95	
50	221525_at	DKFZp761I2123	-1.73	5.84E-08	6.80E-05	-0.49	-5.90	7p12.3
1.4	AML_-7 versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	200976_s_at	TAX1BP1	-1.98	1.86E-16	6.72E-13	-1.52	-16.24	7p15
2	225002_s_at	DKFZP566I1024	-3.00	4.13E-17	1.92E-13	-1.36	-14.89	7q11.1
3	214743_at	CUTL1	-1.94	3.92E-18	2.55E-14	-1.29	-14.50	7q22
4	213893_x_at	PMS2L5	-2.38	1.20E-12	1.22E-09	-1.40	-14.11	7q11-q22
5	226032_at	CASP2	-2.31	1.89E-21	3.08E-17	-1.16	-13.70	7q34-q35
6	224751_at		-2.33	3.91E-15	1.27E-11	-1.23	-13.39	
7	210962_s_at	AKAP9	-2.46	1.07E-12	1.12E-09	-1.25	-12.91	7q21-q22
8	218378_s_at	FLJ13902	-2.62	5.01E-20	5.44E-16	-1.08	-12.78	7q22.1
9	225935_at		-2.44	4.79E-14	8.66E-11	-1.18	-12.71	
10	216843_x_at		-2.07	1.37E-11	1.14E-08	-1.26	-12.63	
11	200977_s_at	TAX1BP1	-2.33	2.79E-10	1.46E-07	-1.31	-12.40	7p15
12	216525_x_at	PMS2L3	-2.07	1.09E-13	1.77E-10	-1.14	-12.30	7q11-q22
13	214526_x_at	PMS2L8	-1.98	2.45E-10	1.33E-07	-1.28	-12.27	7q22

14	225932_s_at		-1.95	7.77E-10	3.24E-07	-1.31	-12.19	
15	209036_s_at	MDH2	-1.97	4.99E-10	2.26E-07	-1.27	-12.01	7p12.3-q11.2
16	214473_x_at	PMS2L9	-2.06	6.09E-11	4.51E-08	-1.21	-11.98	7q11.23
17	201682_at	PMPCB	-1.75	1.47E-13	2.17E-10	-1.09	-11.87	7q22-q32
18	208921_s_at	SRI	-1.83	1.35E-12	1.30E-09	-1.10	-11.70	7q21.1
19	213780_at	THH	-4.44	2.92E-22	9.51E-18	-0.92	-11.48	1q21.3
20	226336_at	PPIA	-2.30	1.34E-08	3.21E-06	-1.31	-11.41	7p13-p11.2
21	213097_s_at	ZRF1	-2.47	4.77E-09	1.49E-06	-1.24	-11.30	7q22-q32
22	217485_x_at	PMS2L1	-2.09	3.24E-08	6.73E-06	-1.32	-11.20	7q11-q22
23	208688_x_at	EIF3S9	-1.82	4.02E-09	1.28E-06	-1.21	-11.13	7p22.3
24	226529_at	FLJ11273	-2.97	9.78E-14	1.68E-10	-1.00	-11.10	7p21.3
25	226386_at	LOC115416	-2.30	9.33E-12	8.00E-09	-1.05	-11.06	7p15.3
26	201317_s_at	PSMA2	-1.69	7.68E-10	3.24E-07	-1.12	-10.93	7p13
27	201327_s_at	CCT6A	-1.98	3.18E-09	1.06E-06	-1.14	-10.78	7p11.1
28	218321_x_at	MK-STYX	-2.62	9.49E-10	3.91E-07	-1.09	-10.65	7q11.23
29	206688_s_at	CPSF4	-1.50	1.31E-12	1.30E-09	-0.97	-10.63	7q22.1
30	225556_at	LOC203547	-1.92	3.36E-11	2.61E-08	-1.00	-10.48	Xq28
31	223065_s_at	STARD3NL	-2.32	8.50E-08	1.51E-05	-1.25	-10.48	7p14-p13
32	214756_x_at	PMS2L8	-1.96	1.66E-07	2.59E-05	-1.30	-10.45	7q22
33	226385_s_at	LOC115416	-2.39	1.54E-08	3.62E-06	-1.15	-10.42	7p15.3
34	219041_s_at	RIP60	-2.38	1.65E-10	9.75E-08	-1.02	-10.41	7q36.1
35	201405_s_at	COPS6	-2.03	1.87E-09	6.78E-07	-1.06	-10.36	7q22.1
36	231365_at	HOXA9	-5.13	3.44E-19	2.80E-15	-0.83	-10.35	7p15-p14
37	235521_at	HOXA3	-7.67	7.87E-15	1.97E-11	-0.89	-10.35	7p15-p14
38	201816_s_at	GBAS	-1.99	6.66E-09	1.89E-06	-1.09	-10.27	7p12
39	202591_s_at	SSBP1	-1.72	2.76E-10	1.46E-07	-1.00	-10.24	7q34
40	217842_at	CGI-59	-2.82	6.98E-10	3.03E-07	-1.00	-10.06	7q34
41	214351_x_at	RPL13	1.36	1.09E-08	2.74E-06	1.05	9.91	16q24.3
42	217809_at	BZW2	-2.34	7.01E-09	1.93E-06	-1.03	-9.91	7p21.1
43	242673_at		-2.09	1.05E-09	4.28E-07	-0.98	-9.87	
44	221073_s_at	CARD4	-1.63	2.37E-09	8.39E-07	-1.00	-9.87	7p15-p14
45	220018_at	HAKAI	-2.24	4.86E-10	2.26E-07	-0.96	-9.83	7q22.2
46	226691_at	KIAA1856	-2.33	1.82E-09	6.66E-07	-0.98	-9.82	7p22.2
47	220099_s_at	CGI-59	-2.14	3.14E-07	4.41E-05	-1.21	-9.80	7q34
48	239896_at		-2.37	4.94E-10	2.26E-07	-0.95	-9.77	
49	207202_s_at	NR1I2	-4.29	1.21E-10	7.41E-08	-0.92	-9.74	3q12-q13.3
50	225238_at		-5.53	1.32E-17	7.17E-14	-0.78	-9.72	
1.5	AML_5q versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	224916_at		-3.59	2.94E-24	3.37E-20	-1.14	-13.74	
2	205366_s_at	HOXB6	-42.75	7.11E-28	2.44E-23	-1.11	-13.61	17q21.3
3	217379_at		-2.18	2.30E-21	1.32E-17	-1.06	-12.75	
4	230872_s_at	DKFZP434B103	-6.25	2.38E-24	3.37E-20	-0.99	-12.26	3p25.3

5	205382_s_at	DF	-5.65	6.70E-16	2.30E-12	-1.06	-12.12	19p13.3
6	228904_at		-7.61	1.12E-23	9.62E-20	-0.98	-12.11	
7	236892_s_at		-12.23	1.19E-21	8.15E-18	-0.92	-11.34	
8	216032_s_at	SDBCAG84	-2.82	1.63E-13	3.72E-10	-1.01	-11.28	20pter-q12
9	239791_at		-10.79	2.81E-19	1.38E-15	-0.91	-11.07	
10	227056_at		-2.01	7.40E-09	6.01E-06	-1.14	-11.04	
11	238021_s_at		-7.94	2.01E-18	8.65E-15	-0.91	-10.95	
12	205601_s_at	HOXB5	-2.79	1.22E-13	2.99E-10	-0.92	-10.50	17q21.3
13	228526_at		-2.92	2.12E-08	1.48E-05	-1.04	-10.14	
14	208717_at	OXA1L	-1.90	2.51E-08	1.72E-05	-1.03	-10.01	14q11.2
15	200093_s_at - HG-U133B	HINT1	-1.76	1.03E-06	0.00035687	-1.13	-9.62	5q31.2
16	211922_s_at	CAT	-4.05	4.67E-17	1.78E-13	-0.77	-9.57	11p13
17	213110_s_at	COL4A5	-5.73	2.15E-15	6.72E-12	-0.79	-9.51	Xq22
18	202113_s_at	SNX2	-2.22	6.44E-08	3.69E-05	-0.98	-9.49	5q23
19	232979_at		-4.08	4.24E-15	1.21E-11	-0.79	-9.46	
20	236091_at		-2.83	8.50E-11	1.08E-07	-0.82	-9.15	
21	224767_at		-3.52	2.13E-07	9.51E-05	-0.96	-9.06	
22	221750_at	HMGCS1	1.67	8.22E-06	0.00173375	1.17	8.99	5p14-p13
23	202593_s_at	MIR16	-1.98	7.30E-12	1.25E-08	-0.77	-8.93	16p12-p11.2
24	223696_at		-2.68	6.01E-11	8.26E-08	-0.79	-8.90	
25	205899_at	CCNA1	-4.85	5.36E-11	8.01E-08	-0.78	-8.82	13q12.3-q13
26	211016_x_at	HSPA4	-1.65	7.08E-08	3.99E-05	-0.88	-8.76	5q31.1-q31.2
27	201635_s_at	FXR1	-2.31	5.28E-10	5.67E-07	-0.79	-8.68	3q28
28	213228_at	PDE8B	1.72	2.25E-05	0.0036917	1.24	8.67	5q13.2
29	233825_s_at	CD99L2	-2.85	1.07E-07	5.58E-05	-0.87	-8.62	Xq28
30	238951_at		-4.92	5.55E-14	1.47E-10	-0.70	-8.60	
31	222422_s_at	NDFIP1	-2.32	4.44E-08	2.83E-05	-0.81	-8.37	5q31.3
32	204082_at	PBX3	-3.92	7.69E-07	0.00027514	-0.89	-8.34	9q33-q34
33	238022_at		-5.59	6.85E-10	7.13E-07	-0.75	-8.33	
34	202259_s_at	CG005	1.82	3.95E-05	0.00554212	1.24	8.30	13q12-q13
35	200982_s_at	ANXA6	-2.98	4.20E-10	4.66E-07	-0.74	-8.30	5q32-q34
36	208629_s_at	HADHA	-2.04	4.67E-09	4.09E-06	-0.73	-7.98	2p23
37	218132_s_at	LENG5	1.55	1.92E-05	0.00341944	1.03	7.97	19q13.4
38	200764_s_at	CTNNA1	-1.84	2.80E-07	0.00011881	-0.80	-7.95	5q31
39	231175_at	FLJ30162	-5.42	4.24E-12	8.58E-09	-0.65	-7.92	6p11.1
40	208843_s_at	GORASP2	1.50	1.06E-05	0.00212501	0.95	7.90	2p24.3-q21.3
41	215559_at	ABCC6	-3.29	2.36E-12	5.07E-09	-0.64	-7.86	16p13.1
42	206967_at	CCNT1	-1.97	4.29E-11	6.71E-08	-0.67	-7.86	12pter-qter
43	244548_at		-3.78	5.77E-11	8.26E-08	-0.66	-7.80	
44	206562_s_at	CSNK1A1	-1.86	2.43E-05	0.00386514	-1.00	-7.77	5q32
45	210844_x_at	CTNNA1	-2.04	3.39E-06	0.00086376	-0.86	-7.76	5q31
46	217751_at	LOC51064	-2.01	3.22E-06	0.00083816	-0.85	-7.74	7q34
47	231736_x_at	MGST1	-2.85	5.04E-06	0.00115495	-0.87	-7.74	12p12.3-p12.1
48	217185_s_at		-1.80	4.62E-06	0.00106649	-0.86	-7.69	
49	214780_s_at	MYO9B	1.34	2.85E-06	0.00077745	0.83	7.68	19p13.1
50	208826_x_at	HINT1	-1.44	7.91E-06	0.0016921	-0.89	-7.67	5q31.2

1.6	AML_9q versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	223865_at	SOX6	-3.00	1.48E-16	3.90E-12	-1.00	-11.56	11p15.3
2	208639_x_at	P5	1.91	5.30E-09	2.25E-06	1.21	11.06	2p25.1
3	201011_at	RPN1	1.79	1.58E-07	2.79E-05	1.31	10.52	3q21.3-q25.2
4	239856_at		-3.16	8.30E-16	1.10E-11	-0.79	-9.58	
5	229836_s_at	NUDT4	-4.23	2.43E-14	1.30E-10	-0.77	-9.17	
6	203938_s_at	TAF1C	1.82	1.43E-06	0.00014118	1.17	9.01	16q24
7	232553_at	PCYT1B	-4.32	3.99E-12	7.51E-09	-0.78	-8.93	Xp22.12
8	217328_at	TRB	-3.72	7.90E-14	3.47E-10	-0.74	-8.88	7q34
9	234703_at	HHLA3	-3.38	3.48E-13	1.15E-09	-0.73	-8.73	1p31.1
10	240464_at		-2.09	3.27E-11	4.26E-08	-0.77	-8.70	
11	228119_at	MGC4126	-3.19	7.90E-15	6.95E-11	-0.70	-8.70	3q29
12	231473_at		-3.56	6.13E-13	1.80E-09	-0.73	-8.67	
13	230778_at		-5.86	2.46E-14	1.30E-10	-0.69	-8.51	
14	200809_x_at	RPL12	-1.18	3.50E-08	9.33E-06	-0.86	-8.51	9q34
15	237401_at	ACTN1	-2.07	6.40E-11	6.50E-08	-0.75	-8.49	14q24
16	230939_at		-2.27	1.01E-08	3.72E-06	-0.82	-8.43	
17	211709_s_at	SCGF	2.25	3.06E-06	0.0002465	1.10	8.41	19q13.3
18	214842_s_at	ALB	-3.25	1.85E-13	6.98E-10	-0.68	-8.34	4q11-q13
19	241575_at		-3.02	1.16E-12	2.78E-09	-0.69	-8.27	
20	232444_at		-3.41	1.23E-11	1.92E-08	-0.69	-8.12	
21	236890_at		-1.98	4.28E-11	4.85E-08	-0.69	-8.05	
22	236208_at		-1.88	1.53E-08	5.12E-06	-0.77	-7.99	
23	207470_at	DKFZp566H0824	-3.31	4.30E-10	3.24E-07	-0.71	-7.95	1p36.22
24	242056_at	TRIM45	-1.88	4.02E-09	1.85E-06	-0.73	-7.93	1p11.2
25	235517_at	MGC29898	-3.50	2.58E-09	1.33E-06	-0.72	-7.89	4p15.32
26	214899_at	LOC284323	-5.60	8.07E-13	2.13E-09	-0.64	-7.87	19q13.13
27	224237_at		-4.88	5.40E-10	3.96E-07	-0.69	-7.84	
28	209058_at	EDF1	1.41	6.40E-06	0.0004165	1.03	7.83	9q34.3
29	240539_at		-2.70	3.83E-09	1.84E-06	-0.72	-7.83	
30	241256_at		-3.26	1.71E-08	5.57E-06	-0.74	-7.80	
31	217740_x_at	RPL7A	-1.21	9.15E-07	0.00010419	-0.87	-7.80	9q34
32	230311_s_at	PRDM6	-2.58	3.29E-12	6.67E-09	-0.64	-7.79	5q23.2
33	201031_s_at	HNRPH1	1.53	7.35E-06	0.00045448	1.02	7.76	5q35.3
34	232651_at		-3.15	2.08E-10	1.72E-07	-0.67	-7.73	
35	236666_s_at		-3.08	1.98E-12	4.35E-09	-0.62	-7.72	
36	205561_at	FLJ12242	-2.14	2.25E-09	1.19E-06	-0.70	-7.72	22q13.1
37	214217_at		-3.52	2.04E-10	1.72E-07	-0.66	-7.69	
38	239875_at	NAB1	-2.24	1.06E-06	0.00011252	-0.85	-7.68	2q32.3-q33
39	244110_at	MLL	-2.64	5.25E-12	9.23E-09	-0.63	-7.67	11q23
40	238116_at	DNCL2B	-2.74	1.51E-09	9.74E-07	-0.68	-7.66	16q23.3
41	235484_at		-2.12	3.35E-06	0.0002658	-0.91	-7.63	

42	211253_x_at	PYY	-2.31	6.45E-09	2.58E-06	-0.70	-7.63	17q21.1
43	229413_s_at	RNF3	-1.94	1.74E-09	1.00E-06	-0.68	-7.62	4p16.3
44	234550_at		-3.90	1.68E-09	1.00E-06	-0.68	-7.60	
45	233990_at	FLJ12886	-3.05	1.92E-09	1.03E-06	-0.68	-7.59	19q13.31
46	244266_at	AKR1C1	-2.57	6.19E-12	1.02E-08	-0.62	-7.59	10p15-p14
47	208736_at	ARPC3	1.45	1.32E-06	0.00013477	0.84	7.56	12q24.11
48	229280_s_at		-3.09	4.08E-09	1.85E-06	-0.68	-7.56	
49	239828_at	FLJ25791	-2.63	3.58E-11	4.29E-08	-0.63	-7.54	6q21
50	200599_s_at	TRA1	1.51	5.44E-06	0.00036803	0.92	7.50	12q24.2-q24.3
1.7	AML_normal versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	213110_s_at	COL4A5	3.11	1.03E-10	3.02E-06	0.56	6.95	Xq22
2	236738_at		3.96	6.07E-10	8.87E-06	0.55	6.68	
3	37462_i_at	SF3A2	-1.34	2.32E-08	0.00015207	-0.53	-6.11	19p13.3-p13.2
4	235753_at		1.82	1.77E-08	0.00015207	0.49	5.98	
5	222742_s_at	FLJ14117	1.52	2.61E-08	0.00015207	0.48	5.89	7q22.1
6	206555_s_at	FLJ20274	-1.34	5.27E-08	0.00022029	-0.50	-5.89	16p13.11
7	224968_at	MGC15407	1.54	3.12E-08	0.00015207	0.48	5.87	2p16.1
8	200061_s_at - HG-U133A	RPS24	1.12	9.27E-08	0.00032854	0.46	5.63	10q22-q23
9	243579_at	MSI2	2.09	1.01E-07	0.00032854	0.45	5.60	17q23.1
10	208886_at	H1F0	-2.32	3.76E-07	0.00064622	-0.52	-5.60	22q13.1
11	203007_x_at	LYPLA1	-1.29	1.75E-07	0.00041084	-0.47	-5.59	8q11.23
12	217870_s_at	UMP-CMPK	-1.37	5.17E-07	0.00083976	-0.53	-5.55	
13	220928_s_at	PRDM16	1.51	1.72E-07	0.00041084	0.45	5.51	1p36.23-p33
14	200923_at	LGALS3BP	2.72	1.76E-07	0.00041084	0.45	5.50	17q25
15	200088_x_at - HG-U133A		1.09	1.86E-07	0.00041084	0.45	5.49	
16	244881_at	LMLN	1.73	1.97E-07	0.00041084	0.45	5.48	3
17	213392_at	GPRC5B	1.56	2.88E-07	0.00052599	0.44	5.40	16p12
18	227985_at		1.70	2.86E-07	0.00052599	0.43	5.37	
19	203110_at	PTK2B	-1.43	8.71E-07	0.00121253	-0.47	-5.32	8p21.1
20	203448_s_at	TERF1	-1.33	8.10E-07	0.00118445	-0.46	-5.30	8q13
21	200602_at	APP	-2.99	1.73E-06	0.0018091	-0.51	-5.26	21q21.3
22	228391_at		1.62	6.00E-07	0.00092406	0.42	5.21	
23	239791_at		2.37	1.14E-06	0.00151278	0.42	5.12	
24	212251_at		-1.24	1.21E-06	0.00153789	-0.42	-5.11	
25	209958_s_at	B1	2.30	1.33E-06	0.00162352	0.41	5.05	7p14
26	200093_s_at - HG-U133B	HINT1	1.28	2.07E-06	0.00202018	0.43	5.04	5q31.2
27	207957_s_at	PRKCB1	-1.55	2.61E-06	0.00230902	-0.44	-5.03	16p11.2
28	207983_s_at	STAG2	-1.46	3.59E-06	0.0030013	-0.46	-5.02	Xq25
29	222011_s_at	TCP1	-1.29	2.71E-06	0.00232999	-0.44	-5.01	6q25-q27
30	224444_s_at	MGC14801	1.82	1.73E-06	0.0018091	0.41	5.00	1q32.2
31	230404_at		1.44	1.59E-06	0.001809	0.40	4.99	

32	226098_at	KIAA1374	1.57	1.61E-06	0.001809	0.40	4.99	3q25.33
33	213792_s_at	INSR	-1.72	3.98E-06	0.00314856	-0.46	-4.99	19p13.3-p13.2
34	219602_s_at	FLJ23403	1.63	1.88E-06	0.00189531	0.40	4.96	18p11.21
35	219923_at	TRIM45	1.27	2.31E-06	0.00217469	0.40	4.93	1p11.2
36	218801_at	UGCGL2	1.92	2.42E-06	0.00220742	0.40	4.92	13q32.1
37	221523_s_at	RAGD	-1.58	5.61E-06	0.00381745	-0.46	-4.91	6q15-q16
38	238147_at	TRIM46	1.53	4.11E-06	0.00315881	0.40	4.82	1q21.3
39	235587_at	LOC202781	1.43	3.80E-06	0.00308555	0.39	4.80	7q36.3
40	218236_s_at	PRKCN	-1.77	6.50E-06	0.00395107	-0.42	-4.79	2p21
41	206042_x_at	SNURF	-1.91	7.70E-06	0.00395107	-0.43	-4.78	15q12
42	235433_at		1.27	5.06E-06	0.0035198	0.40	4.78	
43	204198_s_at	RUNX3	-1.73	7.32E-06	0.00395107	-0.42	-4.78	1p36
44	204044_at	QPRT	1.85	4.39E-06	0.00328779	0.39	4.77	16p12.1
45	225314_at	MGC45416	1.41	4.99E-06	0.0035198	0.39	4.77	4p11
46	237291_at		1.53	4.67E-06	0.00341036	0.38	4.76	
47	214953_s_at	APP	-2.80	1.36E-05	0.00490315	-0.49	-4.75	21q21.3
48	221267_s_at	MGC5244	-1.33	7.65E-06	0.00395107	-0.41	-4.73	19p13.3
49	238058_at		1.61	6.14E-06	0.00390065	0.39	4.71	
50	218200_s_at	NDUFB2	1.32	8.40E-06	0.00409382	0.40	4.70	7q34

Table 2

2. All-Pairs (AP)

2.1	AML_+11 versus AML_+13							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	201462_at	KIAA0193	19.96	4.07E-05	0.05890284	3.37	10.13	7p14.3-p14.1
2	215067_x_at		3.01	2.94E-06	0.03030456	2.45	8.99	
3	220987_s_at	SNARK	-3.59	9.20E-06	0.03104883	-2.44	-8.74	1q32.1
4	208820_at	PTK2	-106.68	0.00013569	0.09287966	-3.19	-8.60	8q24-qter
5	225745_at		-5.31	4.56E-06	0.03030456	-2.30	-8.47	
6	229838_at	NUCB2	3.03	2.30E-05	0.04422077	2.42	8.45	11p15.1-p14
7	232946_s_at		2.27	2.85E-06	0.03030456	2.20	8.24	
8	228910_at	KAI1	3.73	1.34E-05	0.03512847	2.23	8.07	11p11.2
9	223467_at	RASD1	-22.75	0.00018151	0.09722928	-2.78	-8.03	17p11.2
10	230443_at	NHP2L1	4.59	5.19E-06	0.03030456	2.14	7.95	22q13.2-q13.31
11	228046_at	LOC152485	3.41	7.70E-06	0.03030456	2.11	7.81	4q31.1
12	238498_at		3.47	7.74E-06	0.03030456	2.10	7.78	
13	208151_x_at	DDX17	3.02	5.45E-06	0.03030456	2.07	7.73	22q13.1
14	230263_s_at		3.92	7.98E-06	0.03030456	2.01	7.49	
15	219241_x_at	SSH-3	2.15	8.22E-05	0.08757659	2.19	7.49	11q13.1

16	218840_s_at	FLJ10631	2.50	7.37E-05	0.08289974	2.15	7.44	11q13.2
17	230102_at	ETV5	-5.11	0.00013536	0.09287966	-2.21	-7.36	3q28
18	204985_s_at	MGC2650	2.59	1.14E-05	0.03449555	1.96	7.32	19q13.32
19	223960_s_at	C16orf5	2.73	1.39E-05	0.03512847	1.97	7.30	16p13.3
20	219678_x_at	DCLRE1C	1.65	2.57E-05	0.04587637	1.98	7.24	10p13
21	211855_s_at	SLC25A14	3.51	1.69E-05	0.03957268	1.86	6.95	Xq24
22	208855_s_at	STK24	-2.26	2.33E-05	0.04422077	-1.87	-6.91	13q31.2-q32.3
23	230180_at	DDX17	1.77	1.94E-05	0.04203587	1.85	6.90	22q13.1
24	213241_at		-3.28	5.15E-05	0.06902244	-1.90	-6.88	
25	227354_at		-4.65	0.00021335	0.09921257	-2.07	-6.87	
26	203955_at	KIAA0649	10.40	0.00029704	0.10868282	2.08	6.74	9q34.3
27	215580_at		2.95	0.00018916	0.09793849	1.96	6.67	
28	208742_s_at	SAP18	-1.78	0.00015292	0.09287966	-1.93	-6.67	13q11
29	207821_s_at	PTK2	-3.99	0.00016452	0.09399521	-1.93	-6.67	8q24-qter
30	228885_at	MGC21981	17.94	0.00053636	0.11772516	2.34	6.64	9q21.11
31	220925_at	FLJ21613	2.45	0.00010193	0.09287966	1.86	6.63	9q21.33
32	211085_s_at	STK4	2.34	2.97E-05	0.04748544	1.76	6.57	20q11.2-q13.2
33	236208_at		2.49	2.83E-05	0.04748544	1.75	6.56	
34	220041_at	FLJ12768	2.80	3.49E-05	0.05301432	1.72	6.41	3q29
35	203633_at	CPT1A	3.01	5.23E-05	0.06902244	1.72	6.37	11q13.1-q13.2
36	209225_x_at	KPNB2	2.05	5.95E-05	0.07529222	1.72	6.35	5q13.1
37	201952_at	ALCAM	3.93	0.00048745	0.11430437	1.98	6.30	3q13.1
38	213147_at	HOXA10	2.95	6.93E-05	0.08089757	1.70	6.26	7p15-p14
39	211584_s_at	NPAT	3.64	0.00013149	0.09287966	1.74	6.26	11q22-q23
40	200650_s_at	LDHA	1.49	8.36E-05	0.08757659	1.70	6.24	11p15.4
41	224044_at	MIRO-1	3.66	0.00013051	0.09287966	1.73	6.23	17q11.2
42	218856_at	TNFRSF21	-11.19	0.00073245	0.12060164	-2.10	-6.19	6p21.1-12.2
43	223314_at	DC-TM4F2	-2.64	0.00019135	0.09793849	-1.75	-6.17	10q22.3
44	207237_at	KCNA3	-5.22	0.00015258	0.09287966	-1.70	-6.11	1p13.3
45	218909_at	RPS6KC1	2.40	0.00013492	0.09287966	1.68	6.09	1q41
46	232085_at	MAPK8IP3	-2.44	6.46E-05	0.07849066	-1.64	-6.09	16p13.3
47	226764_at	LOC152485	7.40	0.0002907	0.10787089	1.73	6.02	4q31.1
48	213703_at	LOC150759	3.67	0.0001935	0.09793849	1.66	5.96	2q11.1
49	213069_at	KIAA1237	-5.45	0.00025757	0.10028375	-1.68	-5.94	3q21.2
50	238536_at		1.81	0.00015142	0.09287966	1.62	5.91	
2.2	AML_+11 versus AML_+8							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	222490_at	RPC5	2.69	4.79E-08	0.00120568	2.26	9.75	16p12.3
2	242026_at		-1.89	1.70E-07	0.00173969	-2.16	-9.18	
3	228926_s_at	SMARCA2	-1.77	2.83E-07	0.00178171	-2.12	-8.94	9p22.3
4	241234_at		-2.02	2.07E-07	0.00173969	-1.98	-8.55	

5	225595_at		8.64	5.98E-05	0.00996564	2.22	8.07	
6	224132_at	MGC13008	-1.98	1.14E-06	0.00376283	-1.88	-7.95	17p11.2
7	240963_x_at		-1.83	6.23E-07	0.00314182	-1.82	-7.86	
8	242885_at		-1.69	1.22E-06	0.00376283	-1.76	-7.60	
9	240854_x_at		-1.83	9.19E-07	0.00376283	-1.74	-7.58	
10	228910_at	KAI1	3.03	2.16E-05	0.00810641	1.83	7.38	11p11.2
11	232442_at		-1.99	2.82E-06	0.00453973	-1.74	-7.35	
12	226148_at	HSPC063	2.43	2.73E-05	0.00857481	1.82	7.31	11q24.3
13	241454_at		-1.90	1.34E-06	0.00376283	-1.67	-7.27	
14	228519_x_at	CIRBP	-1.85	3.60E-06	0.00453973	-1.72	-7.26	19p13.3
15	228473_at	MSX1	-2.00	2.38E-06	0.00453973	-1.68	-7.20	4p16.3-p16.1
16	242341_x_at	LOC132158	-2.56	1.88E-06	0.00431574	-1.65	-7.18	3p21.31
17	229949_at		2.40	1.38E-05	0.00723256	1.73	7.16	
18	232037_at	PUNC	-1.84	1.68E-06	0.00423186	-1.64	-7.13	15q22.3-q23
19	238569_at	GABBR1	-2.27	7.24E-06	0.00600801	-1.73	-7.11	6p21.31
20	235340_at	CAPN3	-1.67	7.35E-06	0.00600801	-1.68	-7.10	15q15.1-q21.1
21	229118_at	DNCH1	-2.43	3.08E-06	0.00453973	-1.63	-7.06	14q32.3-qter
22	225516_at		-1.95	2.62E-06	0.00453973	-1.63	-7.05	
23	238730_at	ARHGEF11	-5.00	1.11E-05	0.00720104	-1.75	-7.03	1q21
24	229056_at	LOC90313	-3.82	2.38E-06	0.00453973	-1.60	-6.97	17q11.1
25	242353_at		-1.79	3.48E-06	0.00453973	-1.60	-6.93	
26	243230_at		-6.18	1.59E-05	0.00750579	-1.72	-6.86	
27	228646_at	LOC151242	-1.90	4.55E-06	0.00477606	-1.60	-6.86	2q32.1
28	239560_at		-2.08	3.02E-06	0.00453973	-1.58	-6.85	
29	231117_at	LOC90050	-1.82	1.38E-05	0.00723256	-1.68	-6.82	14q32.13
30	236080_at		-2.09	3.64E-06	0.00453973	-1.55	-6.74	
31	243615_at		-1.71	3.78E-06	0.00453973	-1.55	-6.74	
32	232464_at	TRIMP1	-1.97	1.50E-05	0.00750579	-1.65	-6.72	11p15
33	241711_at		-3.80	4.05E-06	0.00461187	-1.53	-6.66	
34	233770_at		-3.70	4.21E-06	0.00461187	-1.52	-6.64	
35	226744_at	MGC3329	2.01	1.29E-05	0.00723256	1.55	6.60	17p13.3
36	205778_at	KLK7	-4.49	1.56E-05	0.00750579	-1.60	-6.59	19q13.33
37	239727_at		-2.13	5.32E-06	0.00535804	-1.50	-6.52	
38	223000_s_at	F11R	2.77	2.96E-05	0.00857481	1.56	6.49	1q21.2-q21.3
39	241131_at		-2.43	6.61E-06	0.00600801	-1.48	-6.44	
40	244003_at		-1.96	7.39E-06	0.00600801	-1.48	-6.43	
41	233965_at	LOC255480	-3.39	1.22E-05	0.00723256	-1.49	-6.41	12q24.21
42	235770_at		-2.20	6.71E-06	0.00600801	-1.47	-6.41	
43	244339_at		-2.09	2.09E-05	0.00798829	-1.54	-6.38	
44	239606_at		-2.62	7.03E-06	0.00600801	-1.46	-6.38	
45	231559_at	NNMT	-2.28	1.03E-05	0.00709721	-1.48	-6.35	11q23.1
46	241189_at		-1.86	1.04E-05	0.00709721	-1.47	-6.32	
47	225719_s_at		-1.80	8.06E-06	0.0063478	-1.44	-6.30	
48	214194_at	DIS3	1.67	1.27E-05	0.00723256	1.46	6.30	13q21.32

49	233285_at		-2.63	8.73E-06	0.00666447	-1.44	-6.27	
50	236349_at		-1.84	1.66E-05	0.0075107	-1.46	-6.26	
2.3	AML_+11 versus AML_-7							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	238498_at		6.90	5.82E-06	0.02583748	3.11	10.98	
2	214756_x_at	PMS2L8	2.05	8.43E-08	0.00160976	2.72	10.74	7q22
3	214526_x_at	PMS2L8	2.03	1.09E-07	0.00160976	2.64	10.47	7q22
4	226336_at	PPIA	2.57	6.98E-06	0.02583748	2.18	8.34	7p13-p11.2
5	227069_at		2.50	5.26E-06	0.02583748	2.13	8.23	
6	214743_at	CUTL1	2.37	0.00010244	0.0844561	2.44	8.07	7q22
7	222796_at	KIAA0632	4.16	3.37E-06	0.02583748	2.05	8.04	7q22.1
8	226344_at	KIAA1789	3.40	4.01E-05	0.06989656	2.21	7.97	Xq21
9	226148_at	HSPC063	2.53	3.43E-05	0.06565541	2.12	7.79	11q24.3
10	221073_s_at	CARD4	1.79	2.76E-05	0.06433243	2.01	7.54	7p15-p14
11	210707_x_at	PMS2L5	2.20	3.04E-05	0.06433243	2.02	7.54	7q11-q22
12	201462_at	KIAA0193	4.11	5.28E-05	0.07443696	2.02	7.39	7p14.3-p14.1
13	229949_at		2.88	5.96E-06	0.02583748	1.84	7.28	
14	216843_x_at		2.16	6.99E-05	0.0793735	1.99	7.24	
15	214473_x_at	PMS2L9	2.43	0.00012438	0.08826335	2.04	7.16	7q11.23
16	217485_x_at	PMS2L1	1.99	1.05E-05	0.03446858	1.82	7.15	7q11-q22
17	225002_s_at	DKFZP566I1024	2.39	4.96E-05	0.07443696	1.91	7.13	7q11.1
18	208073_x_at	TTC3	2.10	6.64E-06	0.02583748	1.76	7.03	21q22.2
19	225595_at		5.20	6.94E-05	0.0793735	1.90	7.02	
20	202591_s_at	SSBP1	1.78	5.90E-05	0.07715011	1.85	6.92	7q34
21	227301_at	CCT6A	4.22	6.56E-05	0.0793735	1.80	6.77	7p11.1
22	219571_s_at	GIOT-3	3.25	0.00026117	0.10233573	1.98	6.71	7p22.2
23	203633_at	CPT1A	2.72	8.57E-05	0.0844561	1.78	6.65	11q13.1-q13.2
24	213147_at	HOXA10	3.27	3.55E-05	0.06565541	1.66	6.48	7p15-p14
25	236533_at	DDEF1	-2.03	2.05E-05	0.06078682	-1.63	-6.44	8q24.1-q24.2
26	210962_s_at	AKAP9	3.93	0.00051017	0.11349014	2.04	6.43	7q21-q22
27	240180_at		3.98	0.00027323	0.10449737	1.82	6.38	
28	222992_s_at	NDUFB9	-1.89	0.00010449	0.0844561	-1.75	-6.38	8q13.3
29	217753_s_at	RPS26	2.03	3.04E-05	0.06433243	1.61	6.36	12q13
30	242026_at		-1.63	6.00E-05	0.07715011	-1.67	-6.35	
31	217969_at	MAGED1	1.87	9.43E-05	0.0844561	1.65	6.27	Xp11.23
32	213151_s_at	CDC10	1.70	8.40E-05	0.0844561	1.64	6.26	7p14.3-p14.1
33	240270_x_at	LOC283728	-1.71	2.97E-05	0.06433243	-1.58	-6.25	15q25.1
34	216525_x_at	PMS2L3	2.49	0.00047679	0.11349014	1.88	6.23	7q11-q22
35	226987_at	HUMAGCGB	1.66	8.40E-05	0.0844561	1.61	6.18	3p21.31
36	205541_s_at	GSPT2	1.97	4.51E-05	0.07411666	1.54	6.08	Xp11.23-p11.21

37	201259_s_at	SYPL	2.06	0.00013642	0.08826335	1.61	6.07	7q22.1
38	225845_at		2.49	0.00043833	0.11349014	1.76	6.06	
39	214100_x_at	WBSCR20C	4.13	0.00043267	0.11349014	1.74	6.04	7q11.23
40	226572_at		1.58	9.37E-05	0.0844561	1.56	6.01	
41	213018_at	ODAG	2.31	0.00022863	0.09998344	1.62	5.98	7q21-q22
42	212079_s_at	MLL	2.80	0.00038932	0.11349014	1.68	5.95	11q23
43	225935_at		2.71	0.00058843	0.11415756	1.76	5.93	
44	200977_s_at	TAX1BP1	2.08	0.00018982	0.09998344	1.57	5.91	7p15
45	224847_at		4.10	0.00044803	0.11349014	1.69	5.91	
46	218601_at	URG4	2.74	7.24E-05	0.0793735	1.50	5.87	7p13
47	209805_at	PMS2	3.21	9.74E-05	0.0844561	1.50	5.85	7p22
48	223162_s_at	LCHN	2.73	0.00014238	0.08826335	1.52	5.83	7q34
49	213670_x_at	WBSCR20C	3.78	0.00022388	0.09998344	1.55	5.80	7q11.23
50	224851_at		5.05	0.00064534	0.11576656	1.71	5.79	
2.4	AML_+11 versus AML_5q							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	214000_s_at	RGS10	-7.27	1.63E-06	0.03266498	-2.91	-10.49	10q25
2	232946_s_at		2.01	1.25E-05	0.03266498	2.66	9.28	
3	201871_s_at	LOC51035	2.48	1.32E-05	0.03266498	2.28	8.21	11q12.2
4	212062_at	ATP9A	-25.77	0.00017878	0.05647163	-2.88	-8.12	20q13.11-q13.2
5	231593_at		-1.86	2.30E-05	0.03266498	-2.23	-7.95	
6	212906_at	KIAA1201	-2.63	7.25E-06	0.03266498	-2.09	-7.77	11q24.1
7	208679_s_at	ARPC2	1.85	2.70E-05	0.03266498	2.15	7.69	2q36.1
8	214863_at		-3.06	9.03E-06	0.03266498	-2.06	-7.65	
9	200005_at - HG-U133B	EIF3S7	2.23	1.30E-05	0.03266498	2.04	7.51	22q13.1
10	212711_at	DKFZp434G2311	-1.55	2.53E-05	0.03266498	-2.07	-7.50	9q34.3
11	214351_x_at	RPL13	1.84	2.37E-05	0.03266498	1.94	7.14	16q24.3
12	236270_at		-1.87	8.18E-05	0.04736438	-2.04	-7.14	
13	230180_at	DDX17	2.13	1.35E-05	0.03266498	1.91	7.13	22q13.1
14	231848_x_at	ZNF207	1.81	1.43E-05	0.03266498	1.91	7.10	17q11.2
15	222047_s_at	ARS2	-1.71	1.50E-05	0.03266498	-1.90	-7.08	7q21
16	208826_x_at	HINT1	1.62	2.99E-05	0.03266498	1.91	7.01	5q31.2
17	229024_at		-3.29	2.52E-05	0.03266498	-1.87	-6.91	
18	235704_at	LOC57228	-2.28	5.96E-05	0.04552235	-1.92	-6.89	12q13.12
19	217379_at		3.37	0.00041827	0.07100828	2.32	6.85	
20	200093_s_at - HG-U133B	HINT1	1.92	5.37E-05	0.04309657	1.89	6.83	5q31.2
21	200093_s_at - HG-U133A	HINT1	1.86	1.85E-05	0.03266498	1.82	6.82	5q31.2
22	217945_at	BTBD1	-1.99	2.05E-05	0.03266498	-1.80	-6.75	15q24
23	222267_at	FLJ14803	-4.36	3.15E-05	0.03292339	-1.82	-6.73	7q32.3
24	229404_at	DERMO1	-2.28	2.34E-05	0.03266498	-1.80	-6.72	2q37.3

25	222527_s_at	FLJ10290	2.90	7.59E-05	0.04714724	1.86	6.68	5q33.1
26	226975_at	FLJ25070	2.76	2.31E-05	0.03266498	1.78	6.67	1p21
27	217528_at	CLCA2	-7.80	0.00049293	0.07463206	-2.21	-6.60	1p31-p22
28	200936_at	RPL8	1.88	5.29E-05	0.04309657	1.79	6.57	8q24.3
29	208728_s_at	CDC42	-2.15	7.65E-05	0.04714724	-1.81	-6.55	1p36.1
30	226835_s_at		2.19	2.89E-05	0.03266498	1.75	6.55	
31	207721_x_at	HINT1	2.05	2.87E-05	0.03266498	1.75	6.54	5q31.2
32	227545_at		-2.62	0.00024646	0.0631726	-1.93	-6.52	
33	200072_s_at - HG-U133A	HNRPM	-1.72	2.96E-05	0.03266498	-1.74	-6.49	19p13.3-p13.2
34	232523_at	MEGF10	-2.87	9.29E-05	0.04736438	-1.79	-6.47	5q33
35	228519_x_at	CIRBP	-1.90	0.00028356	0.06348298	-1.92	-6.45	19p13.3
36	224657_at	MIG-6	-2.66	9.44E-05	0.04736438	-1.78	-6.42	1p36.12-36.33
37	223839_s_at	SCD	-3.30	4.89E-05	0.04202294	-1.74	-6.42	10q23-q24
38	206782_s_at	DNAJC4	3.07	8.98E-05	0.04736438	1.77	6.40	11q13
39	202843_at	DNAJB9	-2.58	4.10E-05	0.03760148	-1.72	-6.40	7q31
40	222501_s_at	RIP60	-2.24	4.22E-05	0.03760148	-1.72	-6.39	7q36.1
41	226236_at	QP-C	1.83	3.72E-05	0.03730714	1.71	6.38	5q31.1
42	240236_at		-3.21	4.13E-05	0.03760148	-1.70	-6.35	
43	211666_x_at	RPL3	1.61	0.00035317	0.06618198	1.91	6.33	22q13
44	221505_at	LANPL	-2.11	6.45E-05	0.04566758	-1.71	-6.31	1q21.2
45	230189_x_at	DKFZP586J1624	-2.16	0.00027091	0.06348298	-1.83	-6.26	9q34.3
46	221002_s_at	DC-TM4F2	-3.10	0.0006878	0.0835569	-2.13	-6.26	10q22.3
47	239489_at		-1.74	0.00013296	0.05113498	-1.75	-6.26	
48	229050_s_at		4.31	0.00027852	0.06348298	1.82	6.25	
49	212874_at	APOE	-2.30	6.36E-05	0.04566758	-1.68	-6.23	19q13.2
50	200072_s_at - HG-U133B	HNRPM	-1.69	7.08E-05	0.04714724	-1.68	-6.21	19p13.3-p13.2
2.5	AML_+11 versus AML_9q							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	218389_s_at	APH-1A	-2.19	1.48E-08	0.00048521	-2.96	-11.79	1p36.13-q31.3
2	222593_s_at	FLJ13117	2.04	2.72E-06	0.01119067	2.47	9.40	12q13.12
3	203168_at	CREBL1	-2.39	2.67E-07	0.00439317	-2.30	-9.19	6p21.3
4	230180_at	DDX17	2.27	9.17E-07	0.01004661	2.19	8.67	22q13.1
5	206851_at	RNASE3	-9.81	3.12E-06	0.01137711	-2.13	-8.27	14q24-q31
6	217780_at	PTD008	-1.65	2.39E-06	0.01119067	-2.06	-8.11	19p13.13
7	208612_at	GRP58	-1.82	4.05E-06	0.01329957	-2.05	-8.02	15q15
8	238498_at		4.16	2.72E-06	0.01119067	2.01	7.94	
9	200080_s_at - HG-U133A	H3F3A	-1.45	1.67E-06	0.01119067	-1.97	-7.87	1q41
10	206111_at	RNASE2	-4.53	2.64E-06	0.01119067	-1.96	-7.80	14q24-q31
11	227082_at		4.79	6.40E-06	0.01583901	1.98	7.73	
12	231300_at	LOC90835	-2.54	7.13E-06	0.01583901	-1.95	-7.57	16p11.2

13	229312_s_at	GKAP42	2.59	2.67E-05	0.02835863	2.00	7.52	9q21.32
14	225595_at		5.95	6.04E-05	0.03179039	2.00	7.30	
15	226975_at	FLJ25070	2.38	3.15E-05	0.03136566	1.92	7.26	1p21
16	220403_s_at	P53AIP1	3.90	1.01E-05	0.01748783	1.84	7.23	11q24
17	222490_at	RPC5	2.08	4.66E-06	0.01391211	1.80	7.20	16p12.3
18	208532_x_at		2.59	1.34E-05	0.01981009	1.86	7.20	
19	222565_s_at	PRKCN	12.61	0.00033804	0.06201888	2.44	7.17	2p21
20	201011_at	RPN1	-2.17	3.54E-05	0.03138737	-1.89	-7.14	3q21.3-q25.2
21	218448_at	C20orf11	-1.95	7.23E-06	0.01583901	-1.78	-7.08	20q13.33
22	223422_s_at	DKFZP564B1162	-3.54	6.08E-06	0.01583901	-1.76	-7.03	4q21.3
23	218376_s_at	MICAL	-3.61	8.29E-06	0.01626704	-1.75	-6.96	6q21
24	216548_x_at		-4.00	4.52E-05	0.03138737	-1.88	-6.93	
25	212973_at	RPIA	-2.65	1.19E-05	0.01858475	-1.75	-6.91	2p11.1
26	200909_s_at	RPLP2	1.31	1.16E-05	0.01858475	1.74	6.88	11p15.5-p15.4
27	236208_at		2.13	5.29E-05	0.03138737	1.81	6.84	
28	210156_s_at	PCMT1	-2.10	8.41E-06	0.01626704	-1.70	-6.82	6q24-q25
29	221488_s_at	LOC51596	-1.56	4.47E-05	0.03138737	-1.83	-6.81	6pter-p21.31
30	218724_s_at	TGIF2	1.82	9.78E-06	0.01748783	1.70	6.80	20q11.2-q12
31	222040_at	HNRPA1	-1.94	1.43E-05	0.01981009	-1.71	-6.78	12q13.1
32	230629_s_at	EP400	2.01	1.97E-05	0.02159747	1.71	6.73	12q24.33
33	218233_s_at	C6orf49	-1.55	1.48E-05	0.01981009	-1.68	-6.67	6p21.31
34	33322_i_at	SFN	-1.28	6.25E-05	0.03208943	-1.76	-6.56	1p35.3
35	213370_s_at	SFMBT	-2.34	5.27E-05	0.03138737	-1.74	-6.56	3p21.31
36	221739_at	IL27w	-1.62	1.64E-05	0.01981009	-1.65	-6.56	19p13.3
37	217927_at	SPC12	-1.57	1.60E-05	0.01981009	-1.64	-6.52	3p21.31
38	214264_s_at	C14orf143	-3.06	5.83E-05	0.03138737	-1.72	-6.49	14q32.11
39	216274_s_at	SPC18	-1.96	3.87E-05	0.03138737	-1.68	-6.47	15q24.3
40	224502_s_at	KIAA1191	1.88	4.19E-05	0.03138737	1.66	6.45	5q35.3
41	203938_s_at	TAF1C	-1.75	1.82E-05	0.02059903	-1.62	-6.45	16q24
42	210042_s_at	CTSZ	-3.94	0.00013984	0.04613013	-1.85	-6.44	20q13
43	201290_at	SPC18	-1.84	1.57E-05	0.01981009	-1.61	-6.44	15q24.3
44	212079_s_at	MLL	3.38	0.00018962	0.05326817	1.79	6.43	11q23
45	210434_x_at	JTB	-1.36	1.69E-05	0.01981009	-1.60	-6.40	1q21
46	208728_s_at	CDC42	-2.14	3.53E-05	0.03138737	-1.62	-6.33	1p36.1
47	229115_at	DNCH1	2.81	0.00010859	0.0443922	1.68	6.33	14q32.3-qter
48	200886_s_at	PGAM1	-2.41	5.14E-05	0.03138737	-1.64	-6.32	10q25.3
49	210161_at	NFATC1	3.85	0.00028368	0.06137512	1.79	6.30	18q23
50	222759_at	CGI-85	1.71	3.66E-05	0.03138737	1.60	6.27	11q13.2
2.6	AML_+11 versus AML_normal							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location

1	205055_at	ITGAE	-2.23	1.85E-12	2.45E-09	-1.23	-11.61	17p13
2	200923_at	LGALS3BP	-12.00	9.95E-19	2.11E-14	-1.04	-10.82	17q25
3	229168_at	DKFZp434K0621	-2.75	5.42E-17	5.74E-13	-0.97	-10.12	5q35.3
4	235749_at	UGCGL2	-6.04	8.26E-14	2.92E-10	-1.00	-10.05	13q32.1
5	214835_s_at	SUCLG2	-6.00	9.69E-10	2.67E-07	-1.11	-10.02	3p14.2
6	212459_x_at	SUCLG2	-5.44	5.06E-09	7.89E-07	-1.11	-9.81	3p14.2
7	230322_at	NFAM1	-2.72	3.21E-14	1.70E-10	-0.96	-9.77	22q13.2
8	219085_s_at	GEMIN7	-3.59	2.43E-12	2.79E-09	-0.97	-9.59	19q13.32
9	238730_at	ARHGEF11	-3.73	1.28E-13	3.88E-10	-0.93	-9.41	1q21
10	242574_at	KIAA0674	-4.30	3.64E-15	2.57E-11	-0.88	-9.21	9q32
11	215772_x_at	SUCLG2	-5.13	1.90E-08	2.19E-06	-1.04	-9.15	3p14.2
12	238058_at		-2.53	1.65E-12	2.33E-09	-0.91	-9.12	
13	216548_x_at		-2.63	1.11E-07	7.94E-06	-1.08	-9.10	
14	225065_x_at	MGC40157	-2.71	6.82E-12	6.28E-09	-0.90	-8.96	17p11.2
15	209706_at	NKX3-1	-2.33	3.70E-11	1.91E-08	-0.90	-8.84	8p21
16	210042_s_at	CTSZ	-3.18	5.29E-14	2.24E-10	-0.84	-8.82	20q13
17	224132_at	MGC13008	-1.65	9.97E-10	2.71E-07	-0.93	-8.81	17p11.2
18	227750_at	TRAD	-1.77	4.16E-13	6.77E-10	-0.86	-8.80	3q21.2
19	201462_at	KIAA0193	5.96	7.41E-05	0.0009482	1.87	8.78	7p14.3-p14.1
20	221002_s_at	DC-TM4F2	-1.86	2.50E-13	6.62E-10	-0.83	-8.60	10q22.3
21	228519_x_at	CIRBP	-1.59	1.26E-09	3.10E-07	-0.91	-8.58	19p13.3
22	242767_at		-2.74	4.78E-12	4.82E-09	-0.84	-8.52	
23	219071_x_at	LOC51236	-1.52	9.72E-08	7.20E-06	-0.96	-8.40	8q24.3
24	212359_s_at	KIAA0913	1.52	2.11E-06	6.98E-05	1.07	8.39	10q22.2
25	217528_at	CLCA2	-4.54	3.23E-13	6.77E-10	-0.80	-8.37	1p31-p22
26	226129_at		-2.23	2.48E-11	1.46E-08	-0.83	-8.36	
27	242345_at		-4.83	2.83E-13	6.66E-10	-0.79	-8.33	
28	230495_at	LOC150568	-4.45	3.77E-13	6.77E-10	-0.79	-8.31	2q12.1
29	232340_at		-1.72	1.74E-09	4.01E-07	-0.87	-8.29	
30	218660_at	DYSF	-4.48	2.85E-09	5.40E-07	-0.88	-8.29	2p13.3-p13.1
31	218389_s_at	APH-1A	-1.74	5.82E-09	8.81E-07	-0.89	-8.28	1p36.13-q31.3
32	223861_at	DKFZP434A1315	-4.12	1.30E-11	1.06E-08	-0.82	-8.27	1q21.2
33	222134_at	DDO	-5.70	4.07E-13	6.77E-10	-0.78	-8.25	6q21
34	228061_at	LOC90693	-2.27	5.35E-08	4.77E-06	-0.92	-8.22	7p15.3
35	205556_at	MSX2	-3.05	3.68E-10	1.28E-07	-0.83	-8.16	5q34-q35
36	232464_at	TRIMP1	-1.69	1.67E-11	1.31E-08	-0.80	-8.10	11p15
37	234974_at	LOC130589	-2.49	2.49E-07	1.42E-05	-0.93	-8.08	2p22.2
38	238263_at		-2.71	3.87E-08	3.79E-06	-0.89	-8.08	
39	231514_at	MGC15882	-2.15	2.50E-12	2.79E-09	-0.77	-8.07	1p34.3
40	235842_at		-3.46	1.43E-10	5.82E-08	-0.81	-8.06	
41	203029_s_at	PTPRN2	-7.26	1.45E-12	2.19E-09	-0.76	-8.02	7q36
42	206962_x_at	NP220	-4.93	2.80E-10	1.00E-07	-0.81	-8.02	2p13.2-

								p13.1
43	204971_at	CSTA	-4.11	1.18E-07	8.27E-06	-0.90	-7.98	3q21
44	242718_at		-2.84	2.78E-11	1.59E-08	-0.78	-7.97	
45	230318_at	SERPINA1	-1.72	6.66E-10	2.02E-07	-0.81	-7.97	14q32.1
46	213823_at	HOXA11	-4.42	8.75E-11	3.94E-08	-0.79	-7.96	7p15-p14
47	224461_s_at	AMID	-6.10	2.05E-12	2.56E-09	-0.75	-7.94	10q22.1
48	239023_at	AF1Q	-2.54	8.61E-12	7.60E-09	-0.77	-7.92	1q21
49	233705_at		-2.22	3.65E-11	1.91E-08	-0.78	-7.90	
50	238498_at		2.62	4.61E-05	0.00067322	1.25	7.86	
2.7	AML_+13 versus AML_+8							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	223467_at	RASD1	11.06	0.00019725	0.09909094	2.30	7.53	17p11.2
2	225365_at	FLJ25952	3.15	6.17E-05	0.0895297	1.94	7.40	13q12.11
3	201908_at	DVL3	-1.69	9.67E-06	0.06972428	-1.63	-6.89	3q27
4	230206_at		-12.73	1.40E-05	0.06972428	-1.66	-6.77	
5	208806_at		1.72	3.43E-06	0.06972428	1.55	6.74	
6	222146_s_at	TCF4	4.06	2.59E-05	0.0895297	1.61	6.67	18q21.1
7	226002_at	GAB1	3.57	0.00034446	0.10862835	1.88	6.52	4q31.1
8	225745_at		2.67	3.10E-05	0.0895297	1.55	6.45	
9	212386_at		5.96	0.00032978	0.1083329	1.82	6.44	
10	201029_s_at	CD99	1.81	1.16E-05	0.06972428	1.49	6.43	Xp22.32
11	239598_s_at	FLJ20481	-4.16	1.33E-05	0.06972428	-1.47	-6.29	16q12.1
12	201717_at	MRPL49	1.46	1.24E-05	0.06972428	1.44	6.24	11q13
13	224681_at	GNA12	4.17	0.00054574	0.11684135	1.86	6.22	7p22-p21
14	242441_at		-2.04	1.50E-05	0.06972428	-1.43	-6.18	
15	229083_at		2.41	0.00041312	0.10886747	1.73	6.16	
16	225157_at	MONDOA	2.10	5.21E-05	0.0895297	1.45	6.05	12q21.31
17	228353_x_at	KIAA1959	2.97	0.00011351	0.09076721	1.44	5.88	11q24.1
18	212387_at		4.08	0.00040982	0.10886747	1.58	5.87	
19	238462_at	KIAA1959	3.84	0.00028469	0.1083329	1.51	5.83	11q24.1
20	207237_at	KCNA3	4.08	0.00022183	0.10519175	1.43	5.70	1p13.3
21	210874_s_at	FUS2	-3.25	2.72E-05	0.0895297	-1.31	-5.70	3p21.3
22	224044_at	MIRO-1	-3.68	4.38E-05	0.0895297	-1.32	-5.65	17q11.2
23	218341_at	FLJ11838	-2.35	4.27E-05	0.0895297	-1.31	-5.62	1p34.1
24	212382_at		3.93	0.00014726	0.09198407	1.35	5.57	
25	235061_at	DKFZp761G058	2.72	0.00016637	0.09888108	1.35	5.54	4q22.1
26	200608_s_at	RAD21	-1.62	3.76E-05	0.0895297	-1.27	-5.52	8q24
27	216266_s_at	BIG1	-2.05	5.14E-05	0.0895297	-1.28	-5.51	8q13
28	227001_at		-4.30	0.00012016	0.09076721	-1.37	-5.50	
29	219013_at	GALNT11	-3.16	3.91E-05	0.0895297	-1.26	-5.50	7q34-q36
30	230207_s_at		-4.59	0.00011072	0.09076721	-1.35	-5.48	
31	218919_at	FLJ14007	-1.73	6.98E-05	0.0895297	-1.29	-5.47	8q21.12
32	227501_at		-3.07	4.25E-05	0.0895297	-1.25	-5.47	

33	216268_s_at	JAG1	-6.62	7.80E-05	0.0895297	-1.30	-5.46	20p12.1-p11.23
34	212688_at	PIK3CB	-2.59	0.00011198	0.09076721	-1.32	-5.42	3q22.3
35	208151_x_at	DDX17	-3.42	7.31E-05	0.0895297	-1.27	-5.40	22q13.1
36	210007_s_at	GPD2	-1.78	5.19E-05	0.0895297	-1.23	-5.36	2q24.1
37	222352_at		2.10	7.10E-05	0.0895297	1.23	5.34	
38	218482_at	DC6	-2.07	0.00019051	0.09909094	-1.36	-5.32	8q23.2
39	202955_s_at	BIG1	-1.70	8.58E-05	0.0895297	-1.25	-5.31	8q13
40	244868_at		-3.53	6.61E-05	0.0895297	-1.22	-5.29	
41	225545_at	EEF2K	-1.49	0.00012622	0.0919415	-1.24	-5.27	16p12.3
42	201848_s_at	BNIP3	-2.06	7.11E-05	0.0895297	-1.21	-5.25	14q11.2-q12
43	204807_at	TMEM5	-2.19	0.00010873	0.09076721	-1.23	-5.25	12q14.1
44	229114_at		3.80	0.00071578	0.12366943	1.39	5.25	
45	214937_x_at	PCM1	-1.86	0.00011605	0.09076721	-1.25	-5.25	8p22-p21.3
46	221949_at	LOC222070	-2.45	8.09E-05	0.0895297	-1.20	-5.20	7p13
47	227696_at	LAT1-3TM	2.29	0.00085878	0.12901585	1.39	5.20	16p12
48	218942_at	FLJ22055	-3.82	7.56E-05	0.0895297	-1.19	-5.19	12q13.13
49	204530_s_at	TOX	2.47	0.00039318	0.10886747	1.29	5.19	8q11.23
50	225789_at	CENTG3	-3.11	7.48E-05	0.0895297	-1.19	-5.18	7q36.1
2.8	AML_+13 versus AML_-7							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	214743_at	CUTL1	1.90	1.50E-06	0.02114767	2.78	10.49	7q22
2	205429_s_at	MPP6	4.19	5.41E-07	0.02007715	2.41	9.49	7p15
3	227459_at		4.48	3.43E-06	0.02114767	2.45	9.31	
4	201816_s_at	GBAS	2.25	9.73E-06	0.03285463	2.13	8.12	7p12
5	226691_at	KIAA1856	2.42	4.82E-06	0.02199787	2.04	7.97	7p22.2
6	217853_at	TEM6	3.92	1.64E-05	0.04691636	2.10	7.93	7p15.1
7	217753_s_at	RPS26	2.01	1.72E-06	0.02114767	1.98	7.90	12q13
8	209036_s_at	MDH2	2.11	2.37E-05	0.05577753	2.10	7.82	7p12.3-q11.2
9	200950_at	ARPC1A	2.33	2.90E-06	0.02114767	1.91	7.62	7q22.1
10	244534_at	ZRF1	1.81	3.99E-06	0.02114767	1.92	7.58	7q22-q32
11	238315_s_at	MGC45586	-4.15	3.51E-06	0.02114767	-1.86	-7.43	19q13.12
12	224681_at	GNA12	7.58	0.00029364	0.13804736	2.34	7.20	7p22-p21
13	211998_at	H3F3B	1.95	5.33E-06	0.02199787	1.78	7.13	17q25
14	222751_at	FLJ22313	2.10	4.57E-05	0.06963876	1.90	7.12	7p14.1
15	225666_at	FLJ14624	2.20	8.72E-06	0.03237276	1.79	7.10	13q32.3
16	208820_at	PTK2	6.85	0.00015736	0.1140083	2.01	7.00	8q24-qter
17	208445_s_at	BAZ1B	3.87	2.31E-05	0.05577753	1.74	6.80	7q11.23
18	209256_s_at	KIAA0265	3.69	9.14E-05	0.0870799	1.84	6.78	7q32.2
19	235061_at	DKFZp761G058	3.06	0.00021332	0.12463041	1.90	6.65	4q22.1
20	224719_s_at	LOC113246	-2.62	1.21E-05	0.03754951	-1.67	-6.65	12p13.31
21	214756_x_at	PMS2L8	2.13	6.96E-05	0.07937861	1.76	6.64	7q22

22	208688_x_at	EIF3S9	1.82	6.92E-05	0.07937861	1.75	6.61	7p22.3
23	213409_s_at	RHEB2	1.80	4.23E-05	0.06963876	1.70	6.57	7q36
24	232231_at		3.90	0.00037911	0.14692205	1.99	6.54	
25	212386_at		5.44	0.00041294	0.14692205	1.92	6.38	
26	223732_at	SLC23A2	3.37	2.40E-05	0.05577753	1.61	6.38	5q31.2-q31.3
27	223065_s_at	STARD3NL	2.21	4.42E-05	0.06963876	1.63	6.37	7p14-p13
28	212074_at	UNC84A	3.60	0.00041146	0.14692205	1.87	6.29	7p22.3
29	221737_at	GNA12	4.20	0.0004951	0.15162063	1.90	6.25	7p22-p21
30	227904_at	FLJ21939	-2.76	4.22E-05	0.06963876	-1.60	-6.24	3p23
31	217028_at	CXCR4	1.63	3.03E-05	0.06254447	1.56	6.20	2q21
32	201338_x_at	GTF3A	1.70	4.00E-05	0.06963876	1.56	6.15	13q12.3-q13.1
33	226694_at	AKAP2	4.70	0.00027279	0.13401821	1.71	6.14	9q31-q33
34	211919_s_at	CXCR4	1.85	2.62E-05	0.05723315	1.53	6.13	2q21
35	233255_s_at	BIVM	-21.14	0.00025967	0.1321119	-1.86	-6.10	13q32-q33.1
36	41220_at	MSF	1.86	0.00011059	0.09335039	1.59	6.07	17q25
37	204021_s_at	PURA	-2.34	5.28E-05	0.07260471	-1.55	-6.06	5q31
38	230207_s_at		-4.61	0.000154	0.1140083	-1.64	-6.00	
39	225775_at		3.06	0.00049805	0.15162063	1.75	5.99	
40	230719_at		4.06	4.69E-05	0.06963876	1.51	5.98	
41	219431_at	FLJ20896	-2.59	0.00011895	0.098173	-1.57	-5.92	4q31.21
42	209201_x_at	CXCR4	1.93	4.21E-05	0.06963876	1.48	5.90	2q21
43	230206_at		-11.89	0.00021017	0.12463041	-1.64	-5.90	
44	222146_s_at	TCF4	2.61	0.00021012	0.12463041	1.57	5.87	18q21.1
45	239213_at	SERPINB1	-3.07	0.00010449	0.09335039	-1.52	-5.85	6p25
46	203462_x_at	EIF3S9	1.57	7.80E-05	0.08271945	1.49	5.84	7p22.3
47	212387_at		3.83	0.00052892	0.15467666	1.68	5.83	
48	203955_at	KIAA0649	-7.84	0.0001992	0.12463041	-1.59	-5.82	9q34.3
49	222352_at		2.38	4.92E-05	0.07026001	1.44	5.78	
50	220239_at	SBBI26	2.41	0.0003991	0.14692205	1.59	5.74	7p15.3
2.9	AML_+13 versus AML_5q							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	230206_at		-13.93	1.96E-05	0.12770447	-2.72	-9.27	
2	217963_s_at	NGFRAP1	-17.98	6.92E-05	0.1331011	-2.91	-9.01	Xq22.1
3	213228_at	PDE8B	-2.49	5.05E-06	0.07226047	-2.19	-8.10	5q13.2
4	227177_at		-5.27	9.97E-05	0.14489136	-2.47	-8.01	
5	225789_at	CENTG3	-3.78	3.86E-06	0.07226047	-2.14	-7.99	7q36.1
6	212889_x_at	PLINP-1	-3.07	6.63E-06	0.07226047	-2.11	-7.85	19p13.12
7	212062_at	ATP9A	-15.13	0.00011017	0.14489136	-2.24	-7.50	20q13.11-q13.2
8	204159_at	CDKN2C	-3.52	4.10E-05	0.12770447	-2.09	-7.45	1p32
9	227490_at	WDFY2	2.25	1.57E-05	0.12770447	2.02	7.42	13q14.12
10	217975_at	LOC51186	-8.30	0.0002654	0.19322144	-2.24	-7.07	Xq22.1

11	206770_s_at	SLC35A3	-1.83	4.09E-05	0.12770447	-1.91	-6.95	1p21
12	238337_s_at		-2.19	2.70E-05	0.12770447	-1.77	-6.61	
13	222664_at	MGC2628	-5.69	0.00024312	0.19322144	-1.88	-6.42	19q13.11
14	201345_s_at	UBE2D2	1.93	4.77E-05	0.12770447	1.73	6.41	5q31.3
15	218926_at	MYNN	-1.83	4.37E-05	0.12770447	-1.72	-6.40	3q26.31
16	215193_x_at	HLA-DRB1	3.09	0.00010775	0.14489136	1.73	6.26	6p21.3
17	202797_at	SACM1L	-2.54	7.69E-05	0.1331011	-1.70	-6.25	3p21.3
18	223374_s_at	B3GALT3	-2.90	5.19E-05	0.12770447	-1.68	-6.24	3q25
19	218198_at	DDX32	-1.66	5.86E-05	0.12770447	-1.67	-6.20	10q26.2
20	225144_at		-3.13	5.15E-05	0.12770447	-1.64	-6.13	
21	202371_at	FLJ21174	-2.43	5.35E-05	0.12770447	-1.64	-6.13	Xq22.1
22	213970_at		-1.79	5.52E-05	0.12770447	-1.63	-6.09	
23	241319_at		-2.23	6.36E-05	0.12994942	-1.62	-6.05	
24	204949_at	ICAM3	-2.10	0.0004088	0.21621427	-1.77	-5.99	19p13.3-p13.2
25	218942_at	FLJ22055	-5.66	0.00024388	0.19322144	-1.69	-5.96	12q13.13
26	226895_at	GEMIN7	-1.68	7.73E-05	0.1331011	-1.59	-5.93	19q13.32
27	230263_s_at		-4.56	0.00027287	0.19402459	-1.68	-5.91	
28	208654_s_at	CD164	-2.48	0.0008185	0.23815977	-1.90	-5.89	6q21
29	243587_x_at		-2.94	9.13E-05	0.14489136	-1.54	-5.77	
30	200651_at	GNB2L1	1.31	9.77E-05	0.14489136	1.54	5.76	5q35.3
31	214313_s_at	IF2	-2.44	0.00011074	0.14489136	-1.53	-5.71	2p11.1-q11.1
32	228073_at	C20orf147	-1.97	0.0001277	0.15821042	-1.50	-5.61	20p11.1
33	203675_at	NUCB2	-2.24	0.00015098	0.15930601	-1.51	-5.59	11p15.1-p14
34	209619_at	CD74	2.05	0.00079496	0.23815977	1.68	5.56	5q32
35	209312_x_at	HLA-DRB1	2.40	0.00014268	0.15821042	1.49	5.55	6p21.3
36	209707_at	PIGK	-2.51	0.0001312	0.15821042	-1.48	-5.53	1p31.1
37	218772_x_at	FLJ10493	-2.57	0.00014231	0.15821042	-1.48	-5.53	9q31.2
38	232744_x_at		-1.84	0.00014511	0.15821042	-1.46	-5.46	
39	237193_s_at		-3.51	0.00050845	0.22419666	-1.54	-5.43	
40	222270_at	KIAA1387	-2.64	0.00025038	0.19322144	-1.47	-5.41	2p16.1
41	202211_at	ARFGAP3	-1.81	0.00017855	0.1825015	-1.45	-5.39	22q13.2-q13.3
42	200602_at	APP	-3.23	0.00074326	0.23815977	-1.57	-5.38	21q21.3
43	200984_s_at	CD59	-2.80	0.00043293	0.22125895	-1.50	-5.36	11p13
44	231869_at	KIAA1586	-1.96	0.0001892	0.18275575	-1.43	-5.35	6p11.1
45	228093_at	FLJ30663	-2.25	0.00020617	0.19216595	-1.44	-5.35	19q13.11
46	209267_s_at	BIGM103	-3.41	0.00119012	0.24482771	-1.65	-5.33	4q22-q24
47	225330_at	MGC18216	-2.82	0.00074848	0.23815977	-1.54	-5.30	15q26.3
48	213076_at	ITPKC	-1.51	0.00021802	0.19273725	-1.42	-5.30	19q13.1
49	229808_at	CHAF1A	-3.12	0.00018997	0.18275575	-1.42	-5.30	19p13.3
50	204011_at	SPRY2	-5.90	0.00094996	0.23815977	-1.57	-5.29	13q22.1
2.1	AML_+13 versus AML_9q							

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	221848_at	KIAA1847	-4.98	1.62E-06	0.00619739	-2.83	-10.38	20q13.3
2	203282_at	GBE1	-5.55	2.41E-06	0.0073763	-2.54	-9.47	3p12.3
3	208653_s_at	CD164	-3.68	7.77E-07	0.00619739	-2.43	-9.44	6q21
4	206851_at	RNASE3	-17.26	5.18E-06	0.01100277	-2.63	-9.42	14q24-q31
5	203168_at	CREBL1	-1.98	1.57E-06	0.00619739	-2.44	-9.31	6p21.3
6	225745_at		4.23	2.68E-05	0.015873	2.65	9.19	
7	231300_at	LOC90835	-3.38	1.92E-06	0.00651427	-2.35	-9.00	16p11.2
8	230207_s_at		-3.91	7.64E-07	0.00619739	-2.20	-8.72	
9	220416_at	KIAA1939	-8.93	1.18E-05	0.0135175	-2.46	-8.71	15q15.3
10	212688_at	PIK3CB	-3.99	1.19E-05	0.0135175	-2.38	-8.54	3q22.3
11	230206_at		-10.62	3.76E-06	0.01045495	-2.17	-8.35	
12	205429_s_at	MPP6	3.85	1.16E-06	0.00619739	2.04	8.17	7p15
13	205084_at	BAP29	-2.97	1.23E-06	0.00619739	-2.03	-8.13	7q22.2
14	228353_x_at	KIAA1959	5.16	7.57E-05	0.02547228	2.36	8.08	11q24.1
15	221923_s_at	NPM1	-1.97	5.72E-06	0.01100277	-2.10	-8.07	5q35
16	205401_at	AGPS	-2.09	1.33E-06	0.00619739	-2.01	-8.02	2q31
17	210156_s_at	PCMT1	-2.78	1.53E-06	0.00619739	-1.99	-7.95	6q24-q25
18	203955_at	KIAA0649	-9.35	1.35E-05	0.01388069	-2.12	-7.89	9q34.3
19	203675_at	NUCB2	-4.23	2.19E-05	0.01523167	-2.06	-7.60	11p15.1-p14
20	222668_at	MGC2628	-10.38	3.39E-05	0.01790158	-2.14	-7.59	19q13.11
21	206111_at	RNASE2	-4.79	5.62E-06	0.01100277	-1.90	-7.49	14q24-q31
22	218743_at	FLJ11749	-6.64	1.92E-05	0.01523167	-2.00	-7.47	17q25.3
23	230263_s_at		-5.38	1.12E-05	0.0135175	-1.92	-7.40	
24	229838_at	NUCB2	-3.16	2.45E-05	0.01563625	-1.99	-7.38	11p15.1-p14
25	210007_s_at	GPD2	-2.21	6.78E-06	0.01220442	-1.86	-7.33	2q24.1
26	204670_x_at	HLA-DRB5	2.87	5.75E-06	0.01100277	1.85	7.31	6p21.3
27	212173_at	AK2	-4.19	3.03E-05	0.01655573	-1.97	-7.28	1p34
28	208626_s_at	VAT1	-2.72	2.25E-05	0.01528447	-1.93	-7.25	17q21
29	218061_at	MEA	-2.26	4.89E-06	0.01100277	-1.80	-7.19	6p21.3-p21.1
30	202371_at	FLJ21174	-3.70	2.13E-05	0.01523167	-1.86	-7.08	Xq22.1
31	224025_s_at	GSA7	-5.62	9.84E-06	0.0135175	-1.78	-7.03	3p25.2
32	221972_s_at	Cab45	-2.04	1.57E-05	0.01501401	-1.79	-7.01	1p36.33
33	209619_at	CD74	2.07	3.14E-05	0.01683547	1.86	6.99	5q32
34	244293_at		2.72	3.74E-05	0.0185198	1.83	6.97	
35	225677_at	BAP29	-2.33	8.57E-06	0.0135175	-1.75	-6.97	7q22.2
36	210150_s_at	LAMA5	-4.79	5.82E-05	0.02192132	-1.93	-6.96	20q13.2-q13.3
37	218840_s_at	FLJ10631	-2.01	1.12E-05	0.0135175	-1.76	-6.93	11q13.2
38	209707_at	PIGK	-3.64	1.17E-05	0.0135175	-1.76	-6.93	1p31.1
39	213896_x_at	KIAA0974	-6.05	2.09E-05	0.01523167	-1.77	-6.86	10q22.2
40	208855_s_at	STK24	2.00	6.03E-05	0.02192132	1.83	6.85	13q31.2-q32.3
41	211733_x_at	SCP2	-1.93	8.03E-06	0.0135175	-1.71	-6.84	1p32
42	209439_s_at	PHKA2	-2.58	1.07E-05	0.0135175	-1.71	-6.81	Xp22.2-

								p22.1
43	224923_at	TTC7	2.13	2.93E-05	0.01640615	1.76	6.80	2p21
44	218942_at	FLJ22055	-3.95	1.78E-05	0.01523167	-1.72	-6.77	12q13.13
45	217780_at	PTD008	-1.86	2.18E-05	0.01523167	-1.71	-6.72	19p13.13
46	222352_at		2.62	1.37E-05	0.01388069	1.69	6.72	
47	222294_s_at		-3.70	2.11E-05	0.01523167	-1.72	-6.71	
48	204561_x_at	APOC2	-32.08	0.00015318	0.03551703	-2.18	-6.69	19q13.2
49	203960_s_at	LOC51668	-2.15	1.14E-05	0.0135175	-1.66	-6.65	1p32.1-p33
50	219431_at	FLJ20896	-2.42	2.38E-05	0.01563625	-1.70	-6.64	4q31.21
2.11	AML_+13 versus AML_normal							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203955_at	KIAA0649	-9.73	1.38E-17	3.28E-14	-1.48	-14.50	9q34.3
2	224839_s_at	GPT2	-12.03	1.89E-24	5.86E-20	-1.26	-13.27	16q12.1
3	233255_s_at	BIVM	-19.05	6.53E-24	1.01E-19	-1.24	-13.03	13q32-q33.1
4	212688_at	PIK3CB	-3.03	9.61E-17	1.65E-13	-1.23	-12.24	3q22.3
5	203949_at	MPO	-11.88	8.84E-22	9.11E-18	-1.16	-12.15	17q23.1
6	217963_s_at	NGFRAP1	-10.94	1.38E-19	6.10E-16	-1.15	-11.87	Xq22.1
7	213110_s_at	COL4A5	-12.87	1.17E-20	9.05E-17	-1.10	-11.56	Xq22
8	220773_s_at	GPHN	-6.32	5.77E-11	1.77E-08	-1.27	-11.51	14q23.3
9	238021_s_at		-10.84	6.53E-20	4.04E-16	-1.09	-11.41	
10	213844_at	HOXA5	-8.12	3.05E-15	3.14E-12	-1.15	-11.38	7p15-p14
11	226763_at	DKFZp434O0515	-4.42	1.38E-11	5.25E-09	-1.23	-11.37	2q31.3
12	208626_s_at	VAT1	-2.50	5.12E-12	2.23E-09	-1.20	-11.29	17q21
13	209267_s_at	BIGM103	-3.54	1.80E-16	2.78E-13	-1.10	-11.14	4q22-q24
14	226141_at		-6.13	1.13E-19	5.82E-16	-1.06	-11.13	
15	227001_at		-3.75	1.66E-13	1.09E-10	-1.13	-11.03	
16	239598_s_at	FLJ20481	-4.78	1.62E-12	8.47E-10	-1.12	-10.76	16q12.1
17	217975_at	LOC51186	-5.80	6.28E-16	8.45E-13	-1.05	-10.68	Xq22.1
18	242476_at		-3.20	5.14E-15	5.13E-12	-1.05	-10.59	
19	203948_s_at	MPO	-16.50	1.96E-18	7.58E-15	-1.00	-10.59	17q23.1
20	219078_at	FLJ10252	-2.64	9.97E-12	3.90E-09	-1.11	-10.52	1q41
21	238784_at	FLJ32949	-8.10	4.94E-18	1.53E-14	-0.99	-	12q14.1

							10.46	
22	230206_at		-9.02	9.10E-12	3.66E-09	-1.10	-10.45	
23	220416_at	KIAA1939	-5.92	2.45E-16	3.61E-13	-1.01	-10.44	15q15.3
24	209739_s_at	DXS1283E	-6.32	4.31E-18	1.48E-14	-0.99	-10.44	Xp22.3
25	232424_at	PRDM16	-28.76	8.62E-18	2.22E-14	-1.01	-10.41	1p36.23-p33
26	200923_at	LGALS3BP	-9.67	6.57E-18	1.85E-14	-0.98	-10.36	17q25
27	223703_at	CDA017	-4.18	6.61E-11	1.95E-08	-1.11	-10.33	10q23.1
28	229838_at	NUCB2	-2.50	8.77E-11	2.49E-08	-1.11	-10.32	11p15.1-p14
29	209619_at	CD74	1.70	1.32E-10	3.42E-08	1.11	10.28	5q32
30	242269_at	DKFZp761G0122	-3.94	1.57E-17	3.46E-14	-0.99	-10.27	1p36.32
31	238022_at		-9.27	2.32E-17	4.48E-14	-0.97	-10.20	
32	205653_at	CTSG	-12.00	1.98E-17	4.08E-14	-0.97	-10.18	14q11.2
33	212173_at	AK2	-3.39	1.37E-12	7.30E-10	-1.04	-10.16	1p34
34	206480_at	LTC4S	-7.43	4.05E-17	7.37E-14	-0.95	-10.03	5q35
35	222664_at	MGC2628	-4.84	1.39E-10	3.59E-08	-1.07	-10.02	19q13.11
36	214575_s_at	AZU1	-11.93	3.03E-15	3.14E-12	-0.96	-9.89	19p13.3
37	216920_s_at	TRGV9	-4.71	2.22E-13	1.40E-10	-0.99	-9.89	7p15
38	212686_at	KIAA1157	-4.26	4.66E-12	2.09E-09	-1.02	-9.88	12q13.3
39	222668_at	MGC2628	-6.65	6.83E-14	5.42E-11	-0.98	-9.86	19q13.11
40	219479_at	KDELC1	-15.03	1.39E-16	2.26E-13	-0.93	-9.81	13q33
41	227711_at	FLJ32942	-6.52	3.02E-15	3.14E-12	-0.95	-9.81	12q13.13
42	204082_at	PBX3	-2.90	7.71E-16	9.94E-13	-0.94	-9.78	9q33-q34
43	219869_s_at	BIGM103	-3.25	1.30E-12	7.04E-10	-0.99	-9.74	4q22-q24
44	239791_at		-4.17	2.65E-16	3.72E-13	-0.92	-9.68	
45	205181_at	ZNF193	-2.89	8.19E-08	9.18E-06	-1.15	-9.57	6p21.3
46	211919_s_at	CXCR4	2.13	9.67E-07	6.96E-05	1.26	9.56	2q21
47	235438_at		-43.51	8.56E-16	1.06E-12	-0.92	-9.52	
48	215806_x_at	TRGC2	-4.76	8.93E-12	3.64E-09	-0.97	-9.51	7p15
49	235749_at	UGCGL2	-6.57	5.09E-11	1.59E-08	-0.98	-9.45	13q32.1
50	236738_at		-45.72	1.33E-15	1.52E-12	-0.91	-9.42	
2.12	AML_+8 versus AML_-7							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	213893_x_at	PMS2L5	2.19	2.18E-07	0.00733489	1.82	8.22	7q11-q22
2	208688_x_at	EIF3S9	1.91	6.94E-07	0.00777901	1.68	7.59	7p22.3
3	214473_x_at	PMS2L9	1.70	6.59E-07	0.00777901	1.64	7.46	7q11.23
4	214526_x_at	PMS2L8	1.85	1.19E-06	0.00841433	1.58	7.16	7q22

5	205778_at	KLK7	5.83	8.08E-06	0.01430348	1.68	7.07	19q13.33
6	238315_s_at	MGC45586	-3.19	1.70E-06	0.00841433	-1.54	-7.01	19q13.12
7	225002_s_at	DKFZP566I1024	3.14	9.11E-06	0.01531866	1.67	7.01	7q11.1
8	203462_x_at	EIF3S9	1.76	1.75E-06	0.00841433	1.53	6.95	7p22.3
9	226336_at	PPIA	2.18	1.66E-06	0.00841433	1.51	6.90	7p13-p11.2
10	203198_at	CDK9	-1.99	1.22E-05	0.01665699	-1.58	-6.81	9q34.1
11	215667_x_at	PMS2L5	1.75	7.87E-06	0.01430348	1.55	6.80	7q11-q22
12	237642_at		1.58	2.81E-06	0.01050728	1.44	6.60	
13	201812_s_at	TOM7	1.67	2.60E-06	0.01050728	1.44	6.59	7p15.3
14	213018_at	ODAG	2.00	3.87E-06	0.01300022	1.40	6.42	7q21-q22
15	217485_x_at	PMS2L1	2.09	6.36E-06	0.01336595	1.43	6.42	7q11-q22
16	205690_s_at	G10	1.84	4.38E-06	0.01336595	1.39	6.37	7q22.1
17	223065_s_at	STARD3NL	2.27	5.37E-06	0.01336595	1.40	6.36	7p14-p13
18	226385_s_at	LOC115416	2.32	6.03E-06	0.01336595	1.40	6.34	7p15.3
19	227651_at	NAC1	-1.52	4.99E-06	0.01336595	-1.38	-6.33	19p13.12
20	220099_s_at	CGI-59	2.09	5.61E-06	0.01336595	1.37	6.26	7q34
21	216843_x_at		1.92	1.29E-05	0.01665699	1.41	6.24	
22	213345_at	NFATC4	-3.72	1.82E-05	0.02180241	-1.38	-6.14	14q11.2
23	212475_at	KIAA0241	2.91	7.56E-06	0.01430348	1.34	6.12	7p15.3
24	213097_s_at	ZRF1	2.69	2.30E-05	0.02672164	1.39	6.08	7q22-q32
25	218200_s_at	NDUFB2	2.19	1.26E-05	0.01665699	1.35	6.08	7q34
26	213360_s_at	POM121	1.86	1.00E-05	0.01604533	1.30	5.97	7q11.23
27	225437_s_at	MGC22916	1.47	1.08E-05	0.01647334	1.30	5.96	7p22.3
28	224416_s_at	EG1	-2.05	4.44E-05	0.04147519	-1.37	-5.93	4p16
29	220261_s_at	ZDHHC4	2.08	1.17E-05	0.01665699	1.29	5.91	7p22.2
30	201327_s_at	CCT6A	2.06	3.51E-05	0.03810111	1.32	5.80	7p11.1
31	234339_s_at	GLTSCR2	-2.07	1.55E-05	0.01931425	-1.25	-5.75	19q13.3
32	214756_x_at	PMS2L8	1.95	2.45E-05	0.02740939	1.28	5.74	7q22
33	218600_at	MGC10986	-2.54	3.88E-05	0.0395214	-1.29	-5.72	17q24.1
34	208445_s_at	BAZ1B	4.90	5.52E-05	0.04581459	1.32	5.68	7q11.23
35	AFFX-r2-Ec-bioC-3_at - HG-U133B		1.51	5.84E-05	0.0467416	1.30	5.64	
36	201973_s_at	CGI-43	1.71	3.64E-05	0.03822342	1.23	5.53	7p22.2
37	226386_at	LOC115416	2.22	7.60E-05	0.05790076	1.26	5.45	7p15.3
38	216525_x_at	PMS2L3	1.71	5.26E-05	0.04534688	1.22	5.44	7q11-q22
39	222512_at	NYREN18	2.06	0.0001203	0.06510059	1.30	5.41	7q36
40	207401_at	PROX1	2.02	4.16E-05	0.04000014	1.18	5.39	1q32.2-q32.3
41	212700_x_at	KIAA0356	-2.20	0.00016598	0.07258404	-1.25	-5.34	17q21.31
42	203630_s_at	COG5	2.21	4.02E-05	0.03976338	1.16	5.32	7q31
43	209256_s_at	KIAA0265	3.55	0.00011592	0.06510059	1.22	5.28	7q32.2
44	203476_at	TPBG	-5.45	0.0005934	0.12935328	-1.46	-5.27	6q14-q15
45	238529_at		1.85	4.71E-05	0.04281822	1.14	5.24	
46	224281_s_at	NEUGRIN	-1.94	0.00012195	0.06510059	-1.18	-5.21	15q26.1
47	200076_s_at - HG-U133B	MGC2749	-1.60	5.08E-05	0.04498625	-1.14	-5.21	19p13.11
48	233070_at		-4.41	0.00019248	0.07465882	-1.21	-5.19	
49	212212_s_at	DKFZP586J0619	1.66	5.59E-05	0.04581459	1.13	5.19	7p22.3

50	222823_at	C9orf12	1.55	0.00011253	0.06510059	1.18	5.19	9q21.33-q22.31
2.13	AML_+8 versus AML_5q							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	228526_at		3.75	1.72E-07	0.00593729	2.05	8.81	
2	208717_at	OXA1L	2.07	7.71E-07	0.0133308	1.78	7.72	14q11.2
3	212062_at	ATP9A	-8.57	0.0001549	0.15425292	-1.97	-7.10	20q13.11-q13.2
4	222548_s_at	FLJ20373	-3.06	6.34E-05	0.12825876	-1.80	-7.02	2q11.2
5	202259_s_at	CG005	-2.10	2.91E-06	0.03358103	-1.60	-6.97	13q12-q13
6	222270_at	KIAA1387	-2.75	0.00040268	0.19612094	-1.91	-6.48	2p16.1
7	201811_x_at	SH3BP5	-3.69	0.00015613	0.15425292	-1.65	-6.36	3p24.3
8	213228_at	PDE8B	-1.77	8.39E-06	0.0725429	-1.46	-6.34	5q13.2
9	202843_at	DNAJB9	-2.58	2.07E-05	0.11125277	-1.48	-6.30	7q31
10	218132_s_at	LENG5	-1.63	1.09E-05	0.07510274	-1.42	-6.17	19q13.4
11	214000_s_at	RGS10	-2.34	2.87E-05	0.11125277	-1.45	-6.14	10q25
12	242957_at	FLJ32009	-3.17	7.76E-05	0.12825876	-1.49	-6.09	11q12.2
13	204567_s_at	ABCG1	-3.10	0.00024124	0.17657599	-1.60	-6.09	21q22.3
14	223556_at	HELLS	-2.21	7.94E-05	0.12825876	-1.47	-6.03	10q24.2
15	205849_s_at	UQCRB	1.55	4.15E-05	0.11950873	1.38	5.89	8q22
16	200936_at	RPL8	1.91	2.90E-05	0.11125277	1.37	5.89	8q24.3
17	218552_at	FLJ10948	2.14	2.63E-05	0.11125277	1.36	5.86	1p32.3
18	234998_at		-1.98	7.72E-05	0.12825876	-1.40	-5.84	
19	204367_at	SP2	-2.13	0.00034505	0.19244637	-1.49	-5.72	17q21.32
20	225621_at	FLJ14511	-2.17	5.75E-05	0.12825876	-1.34	-5.71	9q22.33
21	224899_s_at	DKFZp564K142	-1.80	3.82E-05	0.11950873	-1.32	-5.70	Xq13.1-q13.2
22	215884_s_at	UBQLN2	-1.90	0.00012581	0.15002129	-1.37	-5.66	Xp11.23-p11.1
23	220988_s_at	C1QTNF3	-1.62	3.52E-05	0.11950873	-1.30	-5.63	5p13-p12
24	213951_s_at	HUMGT198A	-2.31	9.09E-05	0.12825876	-1.31	-5.54	17q12-q21
25	208243_s_at	CNR1	-2.09	0.00021934	0.1723817	-1.37	-5.54	6q14-q15
26	226838_at		-2.09	5.07E-05	0.12825876	-1.28	-5.54	
27	210596_at	DKFZp564K142	-2.74	0.00055428	0.21780382	-1.46	-5.51	Xq13.1-q13.2
28	216432_at		-2.56	0.00033304	0.19244637	-1.37	-5.43	
29	223304_at	DKFZp761N0624	-4.42	0.00069069	0.21950376	-1.47	-5.43	7q34
30	209705_at		-1.71	5.63E-05	0.12825876	-1.24	-5.38	
31	211063_s_at	NCK1	-2.02	0.00016579	0.15622988	-1.29	-5.37	3q21
32	202113_s_at	SNX2	2.34	9.17E-05	0.12825876	1.26	5.33	5q23
33	218277_s_at	FLJ22060	-1.97	0.00054159	0.21526498	-1.37	-5.30	17q23.2
34	224473_x_at	KIAA1813	-1.55	0.00012521	0.15002129	-1.24	-5.28	10q24
35	200764_s_at	CTNNA1	1.99	9.27E-05	0.12825876	1.24	5.27	5q31
36	218902_at	NOTCH1	-3.04	0.00116334	0.25626922	-1.50	-5.26	9q34.3
37	222422_s_at	NDFIP1	2.22	7.58E-05	0.12825876	1.22	5.26	5q31.3

38	222527_s_at	FLJ10290	2.25	6.83E-05	0.12825876	1.20	5.23	5q33.1
39	206648_at	HSPC059	-2.52	0.0001025	0.13632478	-1.21	-5.23	19q13.12
40	200864_s_at	RAB11A	-1.82	0.00048437	0.20928167	-1.32	-5.22	15q21.3-q22.31
41	201938_at	CDK2AP1	-2.00	0.00065278	0.21950376	-1.35	-5.20	12q24.31
42	234148_at		4.39	0.00013016	0.15003149	1.24	5.20	
43	208608_s_at	SNTB1	3.64	0.00016716	0.15622988	1.24	5.15	8q23-q24
44	204010_s_at	KRAS2	-2.19	0.00023005	0.17530133	-1.23	-5.13	12p12.1
45	214500_at	H2AFY	3.68	9.03E-05	0.12825876	1.17	5.10	5q31.3-q32
46	217963_s_at	NGFRAP1	-3.37	0.00015071	0.15425292	-1.19	-5.09	Xq22.1
47	207049_at	SCN8A	-1.65	0.0002332	0.17530133	-1.21	-5.09	12q13
48	213337_s_at	SOCS1	-2.37	0.0004857	0.20928167	-1.26	-5.07	16p13.13
49	225710_at		-1.94	0.00039299	0.19612094	-1.24	-5.06	
50	212287_at	JJAZ1	-1.84	0.00083212	0.23019518	-1.31	-5.03	17q11.2
2.14	AML_+8 versus AML_9q							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	231949_at		1.90	9.59E-07	0.01362146	1.62	7.34	
2	242326_at		1.90	1.38E-06	0.01362146	1.59	7.20	
3	201548_s_at	PLU-1	-1.93	8.97E-07	0.01362146	-1.55	-7.12	1q32.1
4	239856_at		3.75	9.26E-06	0.02029114	1.71	7.10	
5	238743_at		1.79	3.54E-06	0.020021	1.53	6.84	
6	235340_at	CAPN3	1.72	5.83E-06	0.020021	1.53	6.80	15q15.1-q21.1
7	226226_at	LOC120224	2.12	1.87E-06	0.01384563	1.49	6.79	11q24.3
8	222125_s_at	PH-4	-1.76	5.54E-06	0.020021	-1.49	-6.68	3p21.31
9	53071_s_at	FLJ22222	-2.23	8.09E-06	0.020021	-1.44	-6.46	17q25.3
10	235297_at		1.58	4.06E-06	0.020021	1.39	6.38	
11	235828_at	LOC153768	1.84	1.71E-05	0.02186351	1.43	6.29	5q32
12	201938_at	CDK2AP1	-1.71	6.97E-06	0.020021	-1.35	-6.19	12q24.31
13	237541_at		2.59	6.68E-06	0.020021	1.34	6.15	
14	230724_s_at	FLJ10726	1.59	1.03E-05	0.02046297	1.36	6.13	11q23.2
15	239641_at		1.74	1.24E-05	0.02127338	1.36	6.12	
16	232932_at		1.62	9.57E-06	0.02029114	1.34	6.10	
17	234272_at		2.17	8.07E-06	0.020021	1.33	6.07	
18	218438_s_at	EG1	-1.80	3.77E-05	0.02733054	-1.37	-5.97	4p16
19	206851_at	RNASE3	-3.81	1.77E-05	0.02186351	-1.31	-5.92	14q24-q31
20	242455_at	POU3F2	1.70	1.19E-05	0.02127338	1.29	5.91	6q16
21	226258_at	LOC196394	2.94	1.59E-05	0.02186351	1.28	5.83	12p11.21
22	233965_at	LOC255480	2.42	1.35E-05	0.02127338	1.27	5.81	12q24.21
23	234250_at		2.49	1.36E-05	0.02127338	1.27	5.81	
24	241263_at		2.29	1.64E-05	0.02186351	1.27	5.78	
25	227764_at	LOC130574	1.53	2.28E-05	0.02511591	1.29	5.78	2q23.3
26	203314_at	PGPL	-1.91	3.44E-05	0.02620716	-1.29	-5.76	Xp22.33
27	244293_at		2.02	1.74E-05	0.02186351	1.26	5.75	

28	204481_at	BRPF1	-1.69	2.61E-05	0.02618493	-1.27	-5.74	3p26-p25
29	241281_at		2.49	2.16E-05	0.02511591	1.25	5.68	
30	216504_s_at	BIGM103	-1.63	2.99E-05	0.02618493	-1.26	-5.68	4q22-q24
31	240430_at		2.10	2.69E-05	0.02618493	1.24	5.60	
32	229301_at	FLJ20618	1.80	2.23E-05	0.02511591	1.22	5.58	22q12.2
33	235016_at		3.02	2.86E-05	0.02618493	1.22	5.53	
34	231623_at	MGC13034	1.68	3.10E-05	0.02618493	1.21	5.51	5q13.1
35	241131_at		1.96	2.72E-05	0.02618493	1.20	5.49	
36	222491_at	FLJ32731	1.81	5.85E-05	0.03156796	1.23	5.48	8p11.1
37	202371_at	FLJ21174	-2.34	0.00015351	0.0343193	-1.30	-5.47	Xq22.1
38	239873_at		2.29	2.84E-05	0.02618493	1.19	5.47	
39	233657_at		2.00	4.05E-05	0.02864427	1.21	5.46	
40	231006_at	MGC44294	1.87	3.05E-05	0.02618493	1.19	5.46	15q26.2
41	234956_at		1.50	3.27E-05	0.02618493	1.19	5.45	
42	208653_s_at	CD164	-2.14	3.19E-05	0.02618493	-1.19	-5.44	6q21
43	228657_at	KIF1B	1.95	9.92E-05	0.03370724	1.27	5.43	1p36.2
44	225992_at	MLLT10	-1.86	0.00010278	0.03370724	-1.25	-5.42	10p12
45	228797_at		1.71	3.53E-05	0.02621602	1.19	5.42	
46	203368_at	CRELD1	-1.63	0.00019483	0.0363707	-1.29	-5.40	3p25.3
47	234721_s_at	P450RAI-2	1.68	6.09E-05	0.03156796	1.21	5.39	2p12
48	214271_x_at	RPL12	1.20	3.35E-05	0.02618493	1.18	5.39	9q34
49	230116_at	LOC90133	1.68	7.30E-05	0.03291746	1.22	5.37	3q26.1
50	234486_at	OR51B2	1.55	5.80E-05	0.03156796	1.18	5.33	11p15
2.15	AML_+8 versus AML_normal							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	200923_at	LGALS3BP	-7.68	2.93E-16	1.09E-11	-0.89	-9.59	17q25
2	213110_s_at	COL4A5	-4.95	1.32E-13	2.46E-09	-0.84	-8.81	Xq22
3	243579_at	MSI2	-4.60	3.71E-12	3.45E-08	-0.78	-8.15	17q23.1
4	206761_at	TACTILE	-8.52	6.16E-13	7.64E-09	-0.76	-8.15	3q13.13
5	225406_at	TWSG1	-2.19	2.14E-09	8.84E-06	-0.86	-8.06	18p11.3
6	212489_at	COL5A1	-4.42	1.41E-11	1.05E-07	-0.70	-7.51	9q34.2-q34.3
7	225238_at		-3.76	3.86E-10	2.05E-06	-0.67	-7.06	
8	211907_s_at	PARD6B	-2.80	1.85E-10	1.15E-06	-0.66	-7.05	20q13.13
9	228654_at	LOC139886	-2.12	5.28E-08	8.87E-05	-0.73	-6.92	Xq11.1
10	225102_at	LOC152009	-2.28	4.20E-08	8.24E-05	-0.71	-6.83	3q21.3
11	225889_at	MGC17922	-1.69	3.86E-08	7.99E-05	-0.70	-6.77	12p12.3
12	219553_at	NME7	-1.79	1.58E-09	7.35E-06	-0.64	-6.74	1q24
13	225240_s_at		-3.03	2.22E-08	5.49E-05	-0.68	-6.71	
14	235124_at		-1.75	9.99E-09	3.10E-05	-0.66	-6.68	
15	220240_s_at	C13orf11	-1.93	1.41E-07	0.00018051	-0.69	-6.54	13q34
16	214436_at	FBXL2	-2.19	7.38E-09	2.50E-05	-0.62	-6.47	3p22.2
17	216412_x_at	IGL	-2.89	1.76E-08	4.68E-05	-0.62	-6.41	22q11.1-q11.2

18	204116_at	IL2RG	-2.26	1.66E-08	4.68E-05	-0.62	-6.41	Xq13.1
19	221286_s_at	PACAP	-6.50	3.99E-09	1.48E-05	-0.59	-6.38	5q23-5q31
20	224968_at	MGC15407	-1.86	1.21E-06	0.00082959	-0.72	-6.33	2p16.1
21	203110_at	PTK2B	1.71	1.81E-05	0.00500612	0.92	6.28	8p21.1
22	215071_s_at	HIST1H2AC	-2.92	3.28E-08	7.18E-05	-0.61	-6.24	6p21.3
23	239623_at		-2.85	9.97E-08	0.00014223	-0.62	-6.21	
24	216554_s_at	ENO1	-1.38	2.33E-07	0.0002475	-0.63	-6.16	1p36.3-p36.2
25	226807_at	FLJ34243	-1.78	5.83E-07	0.00049343	-0.65	-6.13	16q22.3
26	225237_s_at		-2.63	4.54E-07	0.00041181	-0.64	-6.11	
27	209014_at	MAGED1	-1.84	1.03E-07	0.00014223	-0.60	-6.07	Xp11.23
28	212259_s_at	HPIP	-3.27	2.36E-08	5.49E-05	-0.57	-6.05	1q21.3
29	243010_at	MSI2	-2.19	5.48E-08	8.87E-05	-0.58	-6.03	17q23.1
30	212250_at		1.43	2.21E-05	0.0055155	0.84	6.02	
31	220591_s_at	FLJ22843	-1.77	1.54E-06	0.00100254	-0.65	-5.99	Xp11.3
32	231903_x_at	KIAA1501	-2.49	5.42E-08	8.87E-05	-0.56	-5.94	17q21.1
33	237216_at		-3.59	4.97E-08	8.87E-05	-0.56	-5.94	
34	228092_at	CREM	-1.64	9.47E-06	0.0033892	-0.71	-5.86	10p12.1-p11.1
35	222490_at	RPC5	-1.87	5.63E-06	0.00229111	-0.68	-5.86	16p12.3
36	226214_at	MIR16	-1.63	5.42E-07	0.00047991	-0.59	-5.82	16p12-p11.2
37	204468_s_at	TIE	-6.80	7.39E-08	0.00011008	-0.55	-5.82	1p34-p33
38	223506_at	LOC84524	-1.60	1.23E-06	0.00082959	-0.61	-5.81	2q13
39	203007_x_at	LYPLA1	1.56	5.03E-05	0.00967904	0.88	5.80	8q11.23
40	206049_at	SELP	-1.85	1.82E-07	0.00021225	-0.56	-5.80	1q22-q25
41	237291_at		-2.02	2.83E-06	0.00148615	-0.64	-5.79	
42	205910_s_at	CEL	-3.75	6.46E-08	0.00010017	-0.54	-5.79	9q34.3
43	219776_s_at	FLJ11125	-2.28	6.71E-07	0.00053151	-0.59	-5.78	8p21.2
44	236738_at		-3.80	2.59E-07	0.00026771	-0.56	-5.74	
45	218250_s_at	CNOT7	1.41	2.94E-05	0.00666472	0.77	5.73	8p22-p21.3
46	214502_at	HIST1H2BJ	-3.36	2.13E-07	0.00023343	-0.55	-5.73	6p21.33
47	220885_s_at	CENPJ	-1.53	1.99E-06	0.00118417	-0.60	-5.69	13q12.12
48	227860_at	CPXM	-2.83	1.28E-06	0.00085014	-0.59	-5.68	20p12.3-p13
49	221525_at	DKFZp761I2123	-1.85	1.28E-07	0.00016985	-0.53	-5.67	7p12.3
50	208457_at	GABRD	-2.20	3.58E-07	0.00035097	-0.55	-5.65	1p36.3
2.16	AML_-7 versus AML_5q							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	220099_s_at	CGI-59	-2.60	2.08E-08	0.00063297	-2.83	-11.31	7q34
2	213151_s_at	CDC10	-2.22	5.96E-07	0.00604841	-2.85	-10.87	7p14.3-p14.1
3	206860_s_at	FLJ20323	-2.07	4.68E-07	0.00604841	-2.32	-9.19	7p22-p21
4	226032_at	CASP2	-3.04	8.52E-05	0.07236746	-2.63	-8.52	7q34-q35
5	214863_at		-2.74	1.25E-06	0.00951178	-2.02	-8.08	

6	211724_x_at	FLJ20323	-2.05	7.25E-06	0.02361369	-2.06	-7.97	7p22-p21
7	224719_s_at	LOC113246	2.92	5.74E-06	0.02181691	2.05	7.91	12p13.31
8	218601_at	URG4	-3.34	4.02E-06	0.01746048	-2.00	-7.83	7p13
9	214351_x_at	RPL13	1.81	5.81E-05	0.06799131	2.15	7.71	16q24.3
10	242673_at		-1.99	3.63E-06	0.01746048	-1.93	-7.66	
11	222047_s_at	ARS2	-1.84	3.74E-06	0.01746048	-1.91	-7.59	7q21
12	222985_at	YWHAG	-2.45	9.31E-06	0.02361369	-1.95	-7.59	7q11.23
13	201453_x_at	RHEB2	-2.22	8.99E-06	0.02361369	-1.93	-7.54	7q36
14	208882_s_at	DD5	-2.05	2.24E-05	0.04304262	-1.86	-7.16	8q22
15	201258_at	RPS16	1.79	8.56E-05	0.07236746	1.91	6.99	19q13.1
16	200976_s_at	TAX1BP1	-2.03	0.00023039	0.09359719	-2.02	-6.86	7p15
17	200651_at	GNB2L1	1.43	8.06E-06	0.02361369	1.71	6.84	5q35.3
18	229932_at		-3.08	3.41E-05	0.05187159	-1.73	-6.70	
19	218132_s_at	LENG5	-1.76	1.10E-05	0.02563607	-1.67	-6.68	19q13.4
20	201978_s_at	KIAA0141	4.20	2.01E-05	0.04304262	1.69	6.64	5q31.3
21	244534_at	ZRF1	-2.02	3.23E-05	0.05168375	-1.70	-6.61	7q22-q32
22	230426_at	DLD	-1.93	2.98E-05	0.05043907	-1.69	-6.60	7q31-q32
23	213025_at	FLJ20274	-2.19	2.26E-05	0.04304262	-1.67	-6.59	16p13.11
24	212062_at	ATP9A	-6.93	0.00012941	0.09059814	-1.80	-6.58	20q13.11-q13.2
25	213360_s_at	POM121	-2.22	9.50E-05	0.07808389	-1.74	-6.50	7q11.23
26	225932_s_at		-1.97	0.00014647	0.09259903	-1.75	-6.44	
27	214743_at	CUTL1	-2.43	0.00053011	0.10453466	-2.02	-6.38	7q22
28	201816_s_at	GBAS	-2.21	0.00021515	0.09359719	-1.71	-6.22	7p12
29	220018_at	HAKAI	-2.83	0.0003617	0.09694113	-1.79	-6.21	7q22.2
30	200060_s_at - HG-U133A	RNPS1	-1.77	6.29E-05	0.0702532	-1.58	-6.16	16p13.3
31	211746_x_at	PSMA1	-1.50	0.0001248	0.09040982	-1.61	-6.11	11p15.1
32	202843_at	DNAJB9	-2.80	2.98E-05	0.05043907	-1.53	-6.10	7q31
33	224767_at		3.91	5.81E-05	0.06799131	1.57	6.09	
34	200883_at	UQCRC2	2.47	4.91E-05	0.06499391	1.54	6.04	16p12
35	226691_at	KIAA1856	-3.02	0.00044603	0.1028092	-1.75	-6.03	7p22.2
36	201316_at	PSMA2	-1.79	3.97E-05	0.05749664	-1.51	-6.01	7p13
37	222772_at	MEF-2	-2.30	0.00027282	0.09359719	-1.64	-5.97	15q15.2
38	217753_s_at	RPS26	-2.02	7.37E-05	0.07236746	-1.52	-5.95	12q13
39	204871_at	MTERF	-2.44	0.00014797	0.09259903	-1.57	-5.94	7q21-q22
40	223626_x_at	FAM14A	2.19	4.80E-05	0.06499391	1.49	5.92	14q32.13
41	204658_at	HSU53209	-2.56	0.00057939	0.10453466	-1.73	-5.88	7p15.3
42	212826_s_at	SLC25A6	1.58	0.00018009	0.09359719	1.56	5.87	Xp22.32 and Yp
43	212287_at	JJAZ1	-2.16	0.0002794	0.09359719	-1.60	-5.86	17q11.2
44	204591_at	CHL1	-5.20	0.00020269	0.09359719	-1.56	-5.85	3p26.1
45	226336_at	PPIA	-2.34	0.00031398	0.09359719	-1.58	-5.78	7p13-p11.2
46	213097_s_at	ZRF1	-2.38	0.00025521	0.09359719	-1.55	-5.78	7q22-q32
47	216032_s_at	SDBCAG84	3.55	0.00028324	0.09359719	1.64	5.78	20pter-q12
48	209095_at	DLD	-2.71	0.00026188	0.09359719	-1.55	-5.77	7q31-q32
49	200005_at - HG-U133B	EIF3S7	2.08	7.75E-05	0.07236746	1.47	5.77	22q13.1

50	223304_at	DKFZp761N0624	-5.39	0.00053932	0.10453466	-1.65	-5.77	7q34
2.17	AML_-7 versus AML_9q							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	201405_s_at	COPS6	-2.48	6.45E-08	0.0019909	-2.49	-10.34	7q22.1
2	201317_s_at	PSMA2	-1.96	2.02E-07	0.00211186	-2.39	-9.83	7p13
3	220018_at	HAKAI	-2.94	5.64E-07	0.00265722	-2.36	-9.56	7q22.2
4	219041_s_at	RIP60	-3.05	7.89E-07	0.00265722	-2.32	-9.36	7q36.1
5	218389_s_at	APH-1A	-1.91	1.27E-07	0.0019909	-2.11	-8.95	1p36.13-q31.3
6	217720_at	LOC51142	-1.52	4.83E-07	0.00265722	-2.01	-8.45	7p11.1
7	209036_s_at	MDH2	-2.43	5.01E-06	0.00683396	-2.14	-8.38	7p12.3-q11.2
8	201812_s_at	TOM7	-2.01	9.63E-07	0.0027431	-2.00	-8.30	7p15.3
9	226385_s_at	LOC115416	-2.41	4.81E-07	0.00265722	-1.94	-8.20	7p15.3
10	213460_x_at	WBSCR20C	-3.28	1.59E-06	0.00355598	-1.95	-8.08	7q11.23
11	201552_at	LAMP1	-1.98	7.99E-07	0.00265722	-1.83	-7.78	13q34
12	201973_s_at	CGI-43	-1.71	7.99E-07	0.00265722	-1.83	-7.78	7p22.2
13	218378_s_at	FLJ13902	-2.61	1.57E-05	0.01375314	-2.03	-7.76	7q22.1
14	203168_at	CREBL1	-2.11	8.48E-07	0.00265722	-1.83	-7.74	6p21.3
15	213404_s_at	RHEB2	-2.17	1.22E-06	0.00319931	-1.82	-7.69	7q36
16	201260_s_at	SYPL	-2.51	1.78E-06	0.00371753	-1.82	-7.64	7q22.1
17	213151_s_at	CDC10	-1.65	1.34E-06	0.00324192	-1.77	-7.50	7p14.3-p14.1
18	226336_at	PPIA	-2.25	3.14E-06	0.00507147	-1.76	-7.34	7p13-p11.2
19	218321_x_at	MK-STYX	-2.99	1.09E-05	0.01102253	-1.82	-7.32	7q11.23
20	231300_at	LOC90835	-2.84	2.81E-06	0.00507147	-1.73	-7.27	16p11.2
21	208612_at	GRP58	-1.54	2.08E-06	0.00408304	-1.70	-7.22	15q15
22	202961_s_at	ATP5J2	-2.16	2.94E-06	0.00507147	-1.71	-7.21	7q22.1
23	224680_at		-2.59	5.45E-06	0.00711338	-1.71	-7.10	
24	220099_s_at	CGI-59	-2.65	1.58E-05	0.01375314	-1.75	-7.04	7q34
25	90610_at	LRRN1	-1.91	3.24E-06	0.00507147	-1.66	-7.02	7q22
26	202605_at	GUSB	-4.46	5.99E-05	0.0223466	-1.89	-6.97	7q21.11
27	201091_s_at	CBX3	-2.28	4.10E-06	0.00612604	-1.64	-6.92	7p15.2
28	214743_at	CUTL1	-2.15	6.84E-05	0.02306167	-1.89	-6.90	7q22
29	225321_s_at	PILR	-2.89	2.43E-05	0.01695251	-1.73	-6.87	7q22.1
30	217773_s_at	NDUFA4	-1.84	4.66E-06	0.00664005	-1.61	-6.81	7p21.3
31	214526_x_at	PMS2L8	-2.16	3.89E-05	0.01913199	-1.73	-6.75	7q22
32	218008_at	FLJ10099	-1.91	1.96E-05	0.01508056	-1.64	-6.67	7q11.21
33	208688_x_at	EIF3S9	-1.95	2.91E-05	0.01788748	-1.67	-6.66	7p22.3
34	211747_s_at	LSM5	-2.32	6.55E-06	0.00789574	-1.57	-6.65	7p14.3
35	202904_s_at	LSM5	-2.77	1.56E-05	0.01375314	-1.61	-6.62	7p14.3
36	36545_s_at	KIAA0542	-1.84	6.43E-06	0.00789574	-1.56	-6.61	22q12.2
37	208921_s_at	SRI	-2.04	6.90E-05	0.02306167	-1.73	-6.58	7q21.1
38	214351_x_at	RPL13	1.52	3.53E-05	0.01913199	1.65	6.57	16q24.3

39	213360_s_at	POM121	-1.75	7.91E-06	0.00907744	-1.56	-6.57	7q11.23
40	214756_x_at	PMS2L8	-2.10	2.20E-05	0.01587622	-1.60	-6.54	7q22
41	201453_x_at	RHEB2	-2.19	1.97E-05	0.01508056	-1.58	-6.49	7q36
42	213893_x_at	PMS2L5	-2.61	8.63E-05	0.02523169	-1.72	-6.47	7q11-q22
43	220261_s_at	ZDHHC4	-2.38	2.23E-05	0.01587622	-1.57	-6.45	7p22.2
44	202854_at	HPRT1	-1.79	8.11E-06	0.00907744	-1.52	-6.44	Xq26.1
45	224281_s_at	NEUGRIN	2.17	6.62E-05	0.02306167	1.67	6.44	15q26.1
46	226975_at	FLJ25070	2.01	1.26E-05	0.01197301	1.53	6.42	1p21
47	226691_at	KIAA1856	-2.65	5.04E-05	0.02024671	-1.61	-6.39	7p22.2
48	205084_at	BAP29	-1.98	1.01E-05	0.01062844	-1.51	-6.39	7q22.2
49	217485_x_at	PMS2L1	-2.23	3.85E-05	0.01913199	-1.59	-6.39	7q11-q22
50	217934_x_at	STUB1	-1.49	2.62E-05	0.01716175	-1.56	-6.37	16p13.3
2.18	AML_-7 versus AML_normal							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	200976_s_at	TAX1BP1	-2.02	8.13E-18	5.96E-14	-1.68	-16.10	7p15
2	225002_s_at	DKFZP566I1024	-3.00	7.56E-18	5.96E-14	-1.38	-13.69	7q11.1
3	213893_x_at	PMS2L5	-2.41	4.87E-14	8.72E-11	-1.42	-13.29	7q11-q22
4	224751_at		-2.43	6.47E-17	3.48E-13	-1.32	-13.00	
5	225932_s_at		-2.01	1.83E-10	1.20E-07	-1.52	-12.75	
6	214743_at	CUTL1	-1.92	4.49E-18	5.96E-14	-1.22	-12.40	7q22
7	200977_s_at	TAX1BP1	-2.36	4.03E-11	3.16E-08	-1.37	-12.04	7p15
8	216843_x_at		-2.07	1.86E-12	2.31E-09	-1.27	-11.77	
9	226032_at	CASP2	-2.27	4.92E-19	1.58E-14	-1.12	-11.64	7q34-q35
10	210962_s_at	AKAP9	-2.36	2.29E-12	2.67E-09	-1.25	-11.63	7q21-q22
11	214473_x_at	PMS2L9	-2.10	3.42E-12	3.67E-09	-1.23	-11.42	7q11.23
12	225935_at		-2.39	4.85E-14	8.72E-11	-1.16	-11.31	
13	214526_x_at	PMS2L8	-1.97	3.63E-11	3.00E-08	-1.25	-11.25	7q22
14	216525_x_at	PMS2L3	-2.08	2.21E-14	5.08E-11	-1.14	-11.17	7q11-q22
15	218378_s_at	FLJ13902	-2.59	9.25E-18	5.96E-14	-1.05	-10.95	7q22.1
16	208921_s_at	SRI	-1.82	6.14E-13	8.60E-10	-1.10	-10.66	7q21.1
17	209036_s_at	MDH2	-1.92	2.22E-10	1.43E-07	-1.20	-10.66	7p12.3-q11.2
18	217485_x_at	PMS2L1	-2.10	8.51E-09	2.39E-06	-1.31	-10.66	7q11-q22
19	218321_x_at	MK-STYX	-2.73	6.92E-11	5.07E-08	-1.16	-	7q11.23

							10.57	
20	235521_at	HOXA3	-8.64	3.53E-16	1.42E-12	-1.02	-10.52	7p15-p14
21	213097_s_at	ZRF1	-2.47	8.68E-10	4.00E-07	-1.21	-10.51	7q22-q32
22	201682_at	PMPCB	-1.73	1.05E-13	1.71E-10	-1.07	-10.50	7q22-q32
23	226336_at	PPIA	-2.28	2.26E-09	7.93E-07	-1.21	-10.39	7p13-p11.2
24	226529_at	FLJ11273	-3.06	2.56E-14	5.49E-11	-1.03	-10.30	7p21.3
25	226386_at	LOC115416	-2.38	3.95E-13	5.79E-10	-1.03	-10.17	7p15.3
26	239896_at		-2.55	9.59E-12	9.08E-09	-1.07	-10.17	
27	218200_s_at	NDUFB2	-2.16	3.09E-08	7.44E-06	-1.24	-9.98	7q34
28	207202_s_at	NR1I2	-4.58	9.52E-12	9.08E-09	-1.04	-9.97	3q12-q13.3
29	201405_s_at	COPS6	-2.06	3.77E-10	2.21E-07	-1.10	-9.95	7q22.1
30	222742_s_at	FLJ14117	-2.36	5.86E-12	5.90E-09	-1.03	-9.93	7q22.1
31	201327_s_at	CCT6A	-1.95	1.67E-09	6.55E-07	-1.13	-9.92	7p11.1
32	225556_at	LOC203547	-1.97	2.32E-12	2.67E-09	-1.02	-9.91	Xq28
33	201317_s_at	PSMA2	-1.68	2.45E-10	1.52E-07	-1.08	-9.90	7p13
34	214756_x_at	PMS2L8	-1.95	7.68E-08	1.56E-05	-1.26	-9.87	7q22
35	231365_at	HOXA9	-5.62	1.30E-16	5.97E-13	-0.92	-9.76	7p15-p14
36	223065_s_at	STARD3NL	-2.30	2.38E-08	5.89E-06	-1.19	-9.75	7p14-p13
37	208688_x_at	EIF3S9	-1.78	1.75E-09	6.72E-07	-1.10	-9.75	7p22.3
38	214351_x_at	RPL13	1.37	4.62E-09	1.39E-06	1.12	9.72	16q24.3
39	226385_s_at	LOC115416	-2.41	1.93E-09	7.30E-07	-1.10	-9.71	7p15.3
40	206289_at	HOXA4	-3.61	3.73E-11	3.00E-08	-1.00	-9.52	7p15-p14
41	210707_x_at	PMS2L5	-1.92	2.46E-09	8.51E-07	-1.06	-9.45	7q11-q22
42	202591_s_at	SSBP1	-1.72	6.73E-11	5.04E-08	-1.00	-9.44	7q34
43	231175_at	FLJ30162	-9.20	1.79E-15	6.41E-12	-0.89	-9.37	6p11.1
44	206688_s_at	CPSF4	-1.48	2.83E-12	3.15E-09	-0.93	-9.26	7q22.1
45	213780_at	THH	-4.32	2.40E-15	7.73E-12	-0.87	-9.21	1q21.3
46	217809_at	BZW2	-2.33	2.18E-09	7.72E-07	-1.02	-9.21	7p21.1
47	225238_at		-6.27	3.46E-15	1.01E-11	-0.86	-9.14	
48	202605_at	GUSB	-2.50	1.38E-08	3.65E-06	-1.06	-9.13	7q21.11
49	242673_at		-2.08	5.17E-10	2.69E-07	-0.98	-9.08	
50	215667_x_at	PMS2L5	-1.95	4.56E-07	6.56E-05	-1.21	-9.06	7q11-q22
2.19	AML_5q versus AML_9q							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	211709_s_at	SCGF	-7.28	4.04E-08	0.0010563	-2.68	-10.70	19q13.3
2	208736_at	ARPC3	-1.90	2.03E-07	0.00265002	-2.40	-9.56	12q24.11
3	229932_at		3.68	2.21E-05	0.04184486	2.01	7.59	
4	203938_s_at	TAF1C	-1.94	3.77E-06	0.03147165	-1.86	-7.42	16q24

5	236895_at		2.65	6.02E-06	0.03147165	1.83	7.26	
6	212062_at	ATP9A	10.60	0.0001275	0.07302304	2.09	7.25	20q13.11-q13.2
7	217751_at	LOC51064	-2.26	5.47E-06	0.03147165	-1.79	-7.14	7q34
8	237081_at		2.25	7.33E-06	0.03197318	1.72	6.90	
9	202113_s_at	SNX2	-2.45	1.78E-05	0.03872848	-1.76	-6.85	5q23
10	214863_at		2.77	1.06E-05	0.03872848	1.72	6.82	
11	208639_x_at	P5	-2.05	6.27E-05	0.06954987	-1.81	-6.80	2p25.1
12	201978_s_at	KIAA0141	-3.23	1.27E-05	0.03872848	-1.67	-6.67	5q31.3
13	236294_at		2.08	1.72E-05	0.03872848	1.68	6.64	
14	229024_at		2.68	5.60E-05	0.06954987	1.74	6.64	
15	239856_at		3.72	0.00033132	0.08160424	1.99	6.62	
16	206851_at	RNASE3	-4.12	1.74E-05	0.03872848	-1.66	-6.56	14q24-q31
17	208674_x_at	DDOST	-1.87	2.65E-05	0.04612176	-1.67	-6.51	1p36.1
18	200095_x_at-HG-U133A	RPS10	1.34	1.75E-05	0.03872848	1.63	6.47	6p21.31
19	204561_x_at	APOC2	-16.50	0.00018153	0.07375653	-2.00	-6.46	19q13.2
20	240191_at		2.44	4.24E-05	0.05832862	1.66	6.45	
21	227679_at		1.70	4.11E-05	0.05832862	1.60	6.28	
22	208646_at	RPS14	-2.66	2.24E-05	0.04184486	-1.56	-6.24	5q31-q33
23	225383_at	ZNF275	1.83	0.00023398	0.07900011	1.67	6.10	Xq28
24	232781_at		1.65	0.00014723	0.07304442	1.60	6.03	
25	229611_at	LMLN	1.61	3.61E-05	0.05741808	1.51	6.03	3
26	202843_at	DNAJB9	2.02	0.0001727	0.07375653	1.59	5.98	7q31
27	207974_s_at	SKP1A	-1.99	3.73E-05	0.05741808	-1.48	-5.92	5q31
28	201049_s_at	RPS18	1.28	6.07E-05	0.06954987	1.50	5.91	6p21.3
29	231764_at	CHRAC1	1.57	0.00012135	0.07302304	1.52	5.86	8q24.3
30	232491_at		2.73	0.00021262	0.07774032	1.56	5.84	
31	208717_at	OXA1L	-1.99	0.00012086	0.07302304	-1.52	-5.80	14q11.2
32	202298_at	NDUFA1	-2.03	6.86E-05	0.07173477	-1.47	-5.80	Xq24
33	209439_s_at	PHKA2	-1.94	9.28E-05	0.07302304	-1.48	-5.76	Xp22.2-p22.1
34	227056_at		-2.04	0.00014189	0.07302304	-1.51	-5.74	
35	226547_at		2.20	5.26E-05	0.06879866	1.43	5.72	
36	223990_at	DKFZP434G072	2.05	6.38E-05	0.06954987	1.41	5.63	4q22.3
37	218436_at	SIL1	-2.90	9.59E-05	0.07302304	-1.42	-5.62	5q31
38	238963_at	MGC2734	2.61	0.0003599	0.08299265	1.52	5.61	9q33.3
39	231101_at	PPP2R5E	1.88	0.0003787	0.08398121	1.52	5.60	14q23.1
40	243406_at		2.09	0.00013157	0.07302304	1.43	5.59	
41	216032_s_at	SDBCAG84	-2.65	0.00023562	0.07900011	-1.50	-5.58	20pter-q12
42	201432_at	CAT	-1.46	8.93E-05	0.07302304	-1.41	-5.58	11p13
43	224062_x_at	KLK4	2.05	0.00012946	0.07302304	1.43	5.56	19q13.41
44	241319_at		1.93	0.00013054	0.07302304	1.42	5.55	
45	208243_s_at	CNR1	2.14	0.00019833	0.07558457	1.44	5.54	6q14-q15
46	218383_at	C14orf94	-2.01	0.00011671	0.07302304	-1.41	-5.53	14q11.2
47	234998_at		2.30	7.49E-05	0.07302304	1.38	5.53	
48	244751_at	MGC41903	-1.81	0.00018334	0.07375653	-1.44	-5.52	19p13.2
49	200674_s_at	RPL32	1.25	7.81E-05	0.07302304	1.38	5.51	3p25-p24

50	223834_at	B7-H1	2.19	0.00021277	0.07774032	1.43	5.51	9p24
2.20	AML_5q versus AML_normal							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	205366_s_at	HOXB6	-46.05	2.89E-24	1.05E-19	-1.29	-13.35	17q21.3
2	205382_s_at	DF	-6.05	4.63E-17	1.87E-13	-1.21	-12.11	19p13.3
3	228904_at		-8.68	2.93E-21	5.32E-17	-1.12	-11.83	
4	236892_s_at		-14.27	7.16E-21	8.67E-17	-1.11	-11.67	
5	224916_at		-3.56	6.61E-20	5.99E-16	-1.11	-11.58	
6	239791_at		-12.77	8.24E-20	5.99E-16	-1.09	-11.44	
7	238021_s_at		-8.88	2.37E-18	1.44E-14	-1.05	-10.93	
8	205601_s_at	HOXB5	-3.03	3.75E-15	1.24E-11	-1.08	-10.80	17q21.3
9	227056_at		-2.04	8.52E-10	1.26E-06	-1.18	-10.54	
10	200093_s_at - HG-U133B	HINT1	-1.86	1.16E-07	7.42E-05	-1.32	-10.47	5q31.2
11	213110_s_at	COL4A5	-7.11	3.09E-17	1.40E-13	-0.99	-10.31	Xq22
12	230872_s_at	DKFZP434B103	-6.42	2.26E-17	1.17E-13	-0.96	-10.12	3p25.3
13	217379_at		-2.02	7.25E-16	2.63E-12	-0.96	-9.91	
14	228526_at		-2.98	2.10E-09	2.36E-06	-1.05	-9.54	
15	221750_at	HMGCS1	1.76	3.24E-06	0.00099583	1.34	9.49	5p14-p13
16	232979_at		-4.52	4.54E-15	1.37E-11	-0.90	-9.39	
17	216032_s_at	SDBCAG84	-2.75	7.72E-13	1.87E-09	-0.93	-9.35	20pter-q12
18	211016_x_at	HSPA4	-1.74	1.80E-09	2.11E-06	-0.94	-8.78	5q31.1-q31.2
19	202259_s_at	CG005	1.94	1.64E-05	0.00320469	1.36	8.77	13q12-q13
20	213228_at	PDE8B	1.75	1.14E-05	0.00243294	1.27	8.62	5q13.2
21	204082_at	PBX3	-4.34	2.96E-08	2.45E-05	-0.96	-8.60	9q33-q34
22	231175_at	FLJ30162	-5.99	3.40E-13	8.83E-10	-0.83	-8.60	6p11.1
23	223696_at		-2.86	1.12E-11	2.40E-08	-0.84	-8.50	
24	211922_s_at	CAT	-4.37	1.53E-13	4.27E-10	-0.80	-8.44	11p13
25	238022_at		-6.21	4.79E-11	8.70E-08	-0.85	-8.42	
26	205899_at	CCNA1	-5.07	2.98E-11	6.02E-08	-0.84	-8.39	13q12.3-q13
27	236091_at		-2.92	4.29E-11	8.21E-08	-0.84	-8.35	
28	208826_x_at	HINT1	-1.51	8.19E-07	0.00032931	-1.01	-8.31	5q31.2
29	218132_s_at	LENG5	1.61	6.38E-06	0.00165733	1.12	8.26	19q13.4
30	233825_s_at	CD99L2	-2.95	1.60E-08	1.45E-05	-0.89	-8.20	Xq28
31	224767_at		-3.32	4.73E-07	0.00021822	-0.97	-8.19	
32	208717_at	OXA1L	-1.83	2.08E-08	1.83E-05	-0.89	-8.17	14q11.2

33	202113_s_at	SNX2	-2.12	8.10E-08	5.45E-05	-0.90	-8.08	5q23
34	208843_s_at	GORASP2	1.55	3.19E-06	0.00099583	1.02	8.00	2p24.3-q21.3
35	206555_s_at	FLJ20274	1.79	5.58E-05	0.00744015	1.34	7.99	16p13.11
36	202843_at	DNAJB9	2.57	0.00010669	0.01200491	1.56	7.97	7q31
37	222422_s_at	NDFIP1	-2.39	8.38E-09	8.23E-06	-0.83	-7.86	5q31.3
38	224968_at	MGC15407	-1.86	3.85E-08	2.98E-05	-0.85	-7.81	2p16.1
39	238951_at		-5.44	6.65E-12	1.51E-08	-0.74	-7.73	
40	214780_s_at	MYO9B	1.38	3.92E-07	0.00018515	0.88	7.65	19p13.1
41	202593_s_at	MIR16	-2.00	9.71E-11	1.68E-07	-0.74	-7.58	16p12-p11.2
42	212062_at	ATP9A	9.73	0.00025594	0.02209426	2.13	7.57	20q13.11-q13.2
43	212906_at	KIAA1201	2.02	8.82E-05	0.01037328	1.29	7.56	11q24.1
44	202423_at	RUNXBP2	1.81	1.26E-05	0.00263335	1.01	7.55	8p11
45	201635_s_at	FXR1	-2.30	1.26E-09	1.64E-06	-0.76	-7.54	3q28
46	206562_s_at	CSNK1A1	-1.88	1.05E-05	0.002256	-0.99	-7.51	5q32
47	231736_x_at	MGST1	-2.86	2.71E-06	0.00088008	-0.90	-7.42	12p12.3-p12.1
48	208967_s_at	AK2	-2.03	1.07E-09	1.50E-06	-0.74	-7.40	1p34
49	208629_s_at	HADHA	-2.14	1.47E-09	1.84E-06	-0.74	-7.39	2p23
50	217751_at	LOC51064	-2.05	6.95E-07	0.00030083	-0.84	-7.36	7q34
2.21	AML_9q versus AML_normal							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	223865_at	SOX6	-3.19	6.90E-17	1.80E-12	-1.04	-10.73	11p15.3
2	201011_at	RPN1	1.83	5.01E-08	2.00E-05	1.36	10.44	3q21.3-q25.2
3	208639_x_at	P5	1.89	1.59E-09	1.43E-06	1.19	10.29	2p25.1
4	203938_s_at	TAF1C	1.84	5.04E-07	9.69E-05	1.13	8.68	16q24
5	200809_x_at	RPL12	-1.20	1.69E-09	1.47E-06	-0.94	-8.68	9q34
6	229836_s_at	NUDT4	-4.51	1.88E-13	2.44E-09	-0.82	-8.61	
7	201031_s_at	HNRPH1	1.59	2.15E-06	0.00025402	1.11	8.12	5q35.3
8	237401_at	ACTN1	-2.16	3.31E-11	1.37E-07	-0.79	-8.03	14q24
9	239856_at		-3.22	1.77E-12	1.54E-08	-0.76	-8.01	
10	236208_at		-1.97	1.75E-09	1.47E-06	-0.82	-7.91	
11	208736_at	ARPC3	1.51	3.06E-07	7.04E-05	0.94	7.90	12q24.11
12	217328_at	TRB	-3.81	5.94E-12	3.87E-08	-0.75	-7.87	7q34
13	240464_at		-2.06	2.21E-10	3.39E-07	-0.78	-7.79	
14	232553_at	PCYT1B	-4.24	6.80E-11	2.21E-07	-0.76	-7.77	Xp22.12
15	200599_s_at	TRA1	1.57	1.73E-06	0.00021745	1.00	7.76	12q24.2-q24.3
16	211253_x_at	PYY	-2.49	5.84E-10	6.91E-07	-0.78	-7.74	17q21.1
17	209058_at	EDF1	1.41	4.34E-06	0.00039597	1.06	7.70	9q34.3
18	242056_at	TRIM45	-1.97	6.23E-10	7.04E-07	-0.77	-7.67	1p11.2
19	234703_at	HHLA3	-3.40	2.29E-11	1.19E-07	-0.73	-7.65	1p31.1

20	230939_at		-2.31	3.63E-09	2.62E-06	-0.79	-7.63	
21	200088_x_at - HG-U133A		-1.18	6.17E-07	0.00010555	-0.91	-7.58	
22	211709_s_at	SCGF	2.06	4.19E-06	0.00038641	1.02	7.57	19q13.3
23	231473_at		-3.67	3.70E-11	1.37E-07	-0.72	-7.52	
24	235517_at	MGC29898	-3.71	8.50E-10	8.32E-07	-0.75	-7.51	4p15.32
25	238116_at	DNCL2B	-2.97	4.25E-10	5.27E-07	-0.73	-7.39	16q23.3
26	204073_s_at	C11orf9	-3.71	7.38E-09	4.36E-06	-0.76	-7.38	11q12-q13.1
27	201552_at	LAMP1	1.60	7.19E-06	0.00053561	1.02	7.36	13q34
28	200087_s_at - HG-U133A	RNP24	1.45	5.16E-06	0.00043877	0.99	7.36	12q24.31
29	200674_s_at	RPL32	-1.30	6.61E-07	0.00011076	-0.87	-7.36	3p25-p24
30	232651_at		-3.43	1.92E-10	3.32E-07	-0.71	-7.32	
31	217740_x_at	RPL7A	-1.21	2.35E-07	5.83E-05	-0.83	-7.31	9q34
32	239875_at	NAB1	-2.26	4.14E-07	8.62E-05	-0.84	-7.29	2q32.3-q33
33	241256_at		-3.37	7.71E-09	4.45E-06	-0.74	-7.25	
34	232444_at		-3.49	2.23E-10	3.39E-07	-0.69	-7.22	
35	240539_at		-2.79	2.66E-09	2.03E-06	-0.72	-7.21	
36	244110_at	MLL	-2.57	1.22E-10	2.64E-07	-0.68	-7.20	11q23
37	214899_at	LOC284323	-6.24	8.52E-11	2.46E-07	-0.68	-7.18	19q13.13
38	239828_at	FLJ25791	-2.75	1.85E-10	3.32E-07	-0.68	-7.16	6q21
39	244266_at	AKR1C1	-2.84	1.01E-10	2.64E-07	-0.67	-7.15	10p15-p14
40	207668_x_at	P5	1.73	7.19E-06	0.00053561	0.95	7.12	2p25.1
41	228119_at	MGC4126	-3.10	1.19E-10	2.64E-07	-0.67	-7.11	3q29
42	210425_x_at	GOLGIN-67	-2.32	3.76E-10	4.89E-07	-0.68	-7.10	15q11.2
43	223529_at	SYT4	-4.70	4.77E-09	3.26E-06	-0.71	-7.08	18q12.3
44	212039_x_at	RPL3	-1.22	3.67E-08	1.62E-05	-0.74	-7.07	22q13
45	230778_at		-5.67	1.46E-10	2.92E-07	-0.67	-7.07	
46	241575_at		-3.11	2.35E-10	3.39E-07	-0.67	-7.05	
47	214217_at		-3.66	8.98E-10	8.34E-07	-0.68	-7.02	
48	235484_at		-2.05	5.73E-06	0.00046598	-0.91	-7.00	
49	242313_at		-2.70	4.09E-08	1.69E-05	-0.73	-6.99	
50	236890_at		-2.01	8.39E-10	8.32E-07	-0.67	-6.97	

Claims

1. A method for distinguishing AML subtypes with different gene dosages selected from AML-TRI8, AML-TRI11, AML-TRI13, AML-MO7, and/or AML-DEL5q in a sample, the method comprising determining the expression level of markers selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, and/or 2,

wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.1 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.1 having a positive fc value,

is indicative for the presence of AML_+11 when AML_+11 is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.2 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.2 having a positive fc value,

is indicative for the presence of AML_+13 when AML_+13 is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.3 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.3 having a positive fc value,

is indicative for the presence of AML_+8 when AML_+8 is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.4 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.4 having a positive fc value,

is indicative for the presence of AML_-7 when AML_-7 is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.5 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.5 having a positive fc value,

is indicative for the presence of AML_5q when AML_5q is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.6 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.6 having a positive fc value,

is indicative for the presence of AML_9q when AML_9q is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.7 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.7 having a positive fc value,

is indicative for the presence of AML_normal when AML_normal is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.1 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.1 having a positive fc value,

is indicative for the presence of AML_+11 when AML_+11 is distinguished from AML_+13,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.2 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.2 having a positive fc value,

is indicative for the presence of AML_+11 when AML_+11 is distinguished from AML_+8,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.3 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.3 having a positive fc value,

is indicative for the presence of AML_+11 when AML_+11 is distinguished from AML_-7,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.4 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.4 having a positive fc value,

is indicative for the presence of AML_+11 when AML_+11 is distinguished from AML_5q,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.5 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.5 having a positive fc value,

is indicative for the presence of AML_+11 when AML_+11 is distinguished from AML_9q,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.6 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.6 having a positive fc value,

is indicative for the presence of AML_+11 when AML_+11 is distinguished from AML_normal,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.7 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.7 having a positive fc value,

is indicative for the presence of AML_+13 when AML_+13 is distinguished from AML_+8,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.8 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.8 having a positive fc value,

is indicative for the presence of AML_+13 when AML_+13 is distinguished from AML_-7,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.9 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.9 having a positive fc value,

is indicative for the presence of AML_+13 when AML_+13 is distinguished from AML_5q,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.10 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.10 having a positive fc value,

is indicative for the presence of AML_+13 when AML_+13 is distinguished from AML_9q,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.11 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.11 having a positive fc value,

is indicative for the presence of AML_+13 when AML_+13 is distinguished from AML_normal,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.12 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.12 having a positive fc value,

is indicative for the presence of AML_+8 when AML_+8 is distinguished from AML_-7,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.13 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.13 having a positive fc value,

is indicative for the presence of AML_+8 when AML_+8 is distinguished from AML_5q,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.14 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.14 having a positive fc value,

is indicative for the presence of AML_+8 when AML_+8 is distinguished from AML_9q,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.15 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.15 having a positive fc value,

is indicative for the presence of AML_+8 when AML_+8 is distinguished from AML_normal,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.16 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.16 having a positive fc value,

is indicative for the presence of AML_-7 when AML_-7 is distinguished from AML_5q,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.17 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.17 having a positive fc value,

is indicative for the presence of AML_-7 when AML_-7 is distinguished from AML_9q,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.18 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.18 having a positive fc value,

is indicative for the presence of AML_-7 when AML_-7 is distinguished from AML_normal,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.19 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.19 having a positive fc value,

is indicative for the presence of AML_5q when AML_5q is distinguished from AML_9q,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.20 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.20 having a positive fc value,

is indicative for the presence of AML_5q when AML_5q is distinguished from AML_normal,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.21 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.21 having a positive fc value,

is indicative for the presence of AML_9q when AML_9q is distinguished from AML_normal.

2. The method according to claim 1 wherein the polynucleotide is labelled.

3. The method according to claim 1 or 2, wherein the label is a luminescent, preferably a fluorescent label, an enzymatic or a radioactive label.

4. The method according at least one of the claims 1-3, wherein the expression level of at least two, preferably of at least ten, more preferably of at least 25, most preferably of 50 of the markers of at least one of the Tables 1.1-2.21 is determined.

5. The method according to at least one of the claims 1-4, wherein the expression level of markers expressed lower in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold lower, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold lower in the first subtype.

6. The method according to at least one of the claims 1-4, wherein the expression level of markers expressed higher in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold higher, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold higher in the first subtype.

7. The method according to at least one of the claims 1-6, wherein the sample is from an individual having AML.

8. The method according to at least one of the claims 1-7, wherein at least one polynucleotide is in the form of a transcribed polynucleotide, or a portion thereof.

9. The method according to claim 8, wherein the transcribed polynucleotide is a mRNA or a cDNA.

10. The method according to claim 8 or 9, wherein the determining of the expression level comprises hybridizing the transcribed polynucleotide to a complementary polynucleotide, or a portion thereof, under stringent hybridization conditions.

11. The method according to at least one of the claims 1-7, wherein at least one polynucleotide is in the form of a polypeptide, or a portion thereof.

12. The method according to at least one of the claims 8, 9 or 12, wherein the determining of the expression level comprises contacting the polynucleotide or the polypeptide with a compound specifically binding to the polynucleotide or the polypeptide.

13. The method according to claim 12, wherein the compound is an antibody, or a fragment thereof.

14. The method according to at least one of the claims 1-13, wherein the method is carried out on an array.

15. The method according to at least one of the claims 1-14, wherein the method is carried out in a robotics system.

16. The method according to at least one of the claims 1-15, wherein the method is carried out using microfluidics.

17. Use of at least one marker as defined in at least one of the claims 1-3 for the manufacturing of a diagnostic for distinguishing AML subtypes with different gene dosages selected from AML-TRI8, AML-TRI11, AML-TRI13, AML-MO7, and/or AML-DEL5q.

18. The use according to claim 17 for distinguishing AML subtypes with different gene dosages selected from AML-TRI8, AML-TRI11, AML-TRI13, AML-MO7, and/or AML-DEL5q in an individual having AML.

19. A diagnostic kit containing at least one marker as defined in at least one of the claims 1-3 for distinguishing AML subtypes with different gene dosages selected from AML-TRI8, AML-TRI11, AML-TRI13, AML-MO7, and/or AML-DEL5q, in combination with suitable auxiliaries.

20. The diagnostic kit according to claim 19, wherein the kit contains at least one reference for the AML subtypes with different gene dosages selected from AML-TRI8, AML-TRI11, AML-TRI13, AML-MO7, and/or AML-DEL5q.

21. The diagnostic kit according to claim 20, wherein the reference is a sample or a data bank.

22. An apparatus for distinguishing AML subtypes with different gene dosages selected from AML-TRI8, AML-TRI11, AML-TRI13, AML-MO7, and/or AML-DEL5q in a sample containing a reference data bank.

23. The apparatus according to claim 22, wherein the reference data bank is obtainable by comprising

(a) compiling a gene expression profile of a patient sample by determining the expression level of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, and/or 2, and

(b) classifying the gene expression profile by means of a machine learning algorithm.

24. The apparatus according to claim 23, wherein the machine learning algorithm is selected from the group consisting of Weighted Voting, K-Nearest Neighbors, Decision Tree Induction, Support Vector Machines, and Feed-Forward Neural Networks, preferably Support Vector Machines.

25. The apparatus according to at least one of the claims 22-24, wherein the apparatus contains a control panel and/or a monitor.

26. A reference data bank for distinguishing AML subtypes with different gene dosages selected from AML-TRI8, AML-TRI11, AML-TRI13, AML-MO7, and/or AML-DEL5q obtainable by comprising
    (a) compiling a gene expression profile of a patient sample by determining the expression level of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, and/or 2, and
    (b) classifying the gene expression profile by means of a machine learning algorithm.

27. The reference data bank according to claim 26, wherein the reference data bank is backed up and/or contained in a computational memory chip.